

11 report sent to the Director of the FBI, Washington, D.C., on 8/1/01.
 12
 13
 14
 15
 16
 17
 18
 19
 20
 21
 22
 23
 24
 25
 26
 27
 28
 29
 30
 31
 32
 33
 34
 35
 36
 37
 38
 39
 40
 41
 42
 43
 44
 45
 46
 47
 48
 49
 50
 51
 52
 53
 54
 55
 56
 57
 58
 59
 60
 61
 62
 63
 64
 65
 66
 67
 68
 69
 70
 71
 72
 73
 74
 75
 76
 77
 78
 79
 80
 81
 82
 83
 84
 85
 86
 87
 88
 89
 90
 91
 92
 93
 94
 95
 96
 97
 98
 99
 100
 101
 102
 103
 104
 105
 106
 107
 108
 109
 110
 111
 112
 113
 114
 115
 116
 117
 118
 119
 120
 121
 122
 123
 124
 125
 126
 127
 128
 129
 130
 131
 132
 133
 134
 135
 136
 137
 138
 139
 140
 141
 142
 143
 144
 145
 146
 147
 148
 149
 150
 151
 152
 153
 154
 155
 156
 157
 158
 159
 160
 161
 162
 163
 164
 165
 166
 167
 168
 169
 170
 171
 172
 173
 174
 175
 176
 177
 178
 179
 180
 181
 182
 183
 184
 185
 186
 187
 188
 189
 190
 191
 192
 193
 194
 195
 196
 197
 198
 199
 200
 201
 202
 203
 204
 205
 206
 207
 208
 209
 210
 211
 212
 213
 214
 215
 216
 217
 218
 219
 220
 221
 222
 223
 224
 225
 226
 227
 228
 229
 230
 231
 232
 233
 234
 235
 236
 237
 238
 239
 240
 241
 242
 243
 244
 245
 246
 247
 248
 249
 250
 251
 252
 253
 254
 255
 256
 257
 258
 259
 260
 261
 262
 263
 264
 265
 266
 267
 268
 269
 270
 271
 272
 273
 274
 275
 276
 277
 278
 279
 280
 281
 282
 283
 284
 285
 286
 287
 288
 289
 290
 291
 292
 293
 294
 295
 296
 297
 298
 299
 300
 301
 302
 303
 304
 305
 306
 307
 308
 309
 310
 311
 312
 313
 314
 315
 316
 317
 318
 319
 320
 321
 322
 323
 324
 325
 326
 327
 328
 329
 330
 331
 332
 333
 334
 335
 336
 337
 338
 339
 340
 341
 342
 343
 344
 345
 346
 347
 348
 349
 350
 351
 352
 353
 354
 355
 356
 357
 358
 359
 360
 361
 362
 363
 364
 365
 366
 367
 368
 369
 370
 371
 372
 373
 374
 375
 376
 377
 378
 379
 380
 381
 382
 383
 384
 385
 386
 387
 388
 389
 390
 391
 392
 393
 394
 395
 396
 397
 398
 399
 400
 401
 402
 403
 404
 405
 406
 407
 408
 409
 410
 411
 412
 413
 414
 415
 416
 417
 418
 419
 420
 421
 422
 423
 424
 425
 426
 427
 428
 429
 430
 431
 432
 433
 434
 435
 436
 437
 438
 439
 440
 441
 442
 443
 444
 445
 446
 447
 448
 449
 450
 451
 452
 453
 454
 455
 456
 457
 458
 459
 460
 461
 462
 463
 464
 465
 466
 467
 468
 469
 470
 471
 472
 473
 474
 475
 476
 477
 478
 479
 480
 481
 482
 483
 484
 485
 486
 487
 488
 489
 490
 491
 492
 493
 494
 495
 496
 497
 498
 499
 500
 501
 502
 503
 504
 505
 506
 507
 508
 509
 510
 511
 512
 513
 514
 515
 516
 517
 518
 519
 520
 521
 522
 523
 524
 525
 526
 527
 528
 529
 530
 531
 532
 533
 534
 535
 536
 537
 538
 539
 540
 541
 542
 543
 544
 545
 546
 547
 548
 549
 550
 551
 552
 553
 554
 555
 556
 557
 558
 559
 560
 561
 562
 563
 564
 565
 566
 567
 568
 569
 570
 571
 572
 573
 574
 575
 576
 577
 578
 579
 580
 581
 582
 583
 584
 585
 586
 587
 588
 589
 590
 591
 592
 593
 594
 595
 596
 597
 598
 599
 600
 601
 602
 603
 604
 605
 606
 607
 608
 609
 610
 611
 612
 613
 614
 615
 616
 617
 618
 619
 620
 621
 622
 623
 624
 625
 626
 627
 628
 629
 630
 631
 632
 633
 634
 635
 636
 637
 638
 639
 640
 641
 642
 643
 644
 645
 646
 647
 648
 649
 650
 651
 652
 653
 654
 655
 656
 657
 658
 659
 660
 661
 662
 663
 664
 665
 666
 667
 668
 669
 670
 671
 672
 673
 674
 675
 676
 677
 678
 679
 680
 681
 682
 683
 684
 685
 686
 687
 688
 689
 690
 691
 692
 693
 694
 695
 696
 697
 698
 699
 700
 701
 702
 703
 704
 705
 706
 707
 708
 709
 710
 711
 712
 713
 714
 715
 716
 717
 718
 719
 720
 721
 722
 723
 724
 725
 726
 727
 728
 729
 730
 731
 732
 733
 734
 735
 736
 737
 738
 739
 740
 741
 742
 743
 744
 745
 746
 747
 748
 749
 750
 751
 752
 753
 754
 755
 756
 757
 758
 759
 760
 761
 762
 763
 764
 765
 766
 767
 768
 769
 770
 771
 772
 773
 774
 775
 776
 777
 778
 779
 780
 781
 782
 783
 784
 785
 786
 787
 788
 789
 790
 791
 792
 793
 794
 795
 796
 797
 798
 799
 800
 801
 802
 803
 804
 805
 806
 807
 808
 809
 810
 811
 812
 813
 814
 815
 816
 817
 818
 819
 820
 821
 822
 823
 824
 825
 826
 827
 828
 829
 830
 831
 832
 833
 834
 835
 836
 837
 838
 839
 840
 841
 842
 843
 844
 845
 846
 847
 848
 849
 850
 851
 852
 853
 854
 855
 856
 857
 858
 859
 860
 861
 862
 863
 864
 865
 866
 867
 868
 869
 870
 871
 872
 873
 874
 875
 876
 877
 878
 879
 880
 881
 882
 883
 884
 885
 886
 887
 888
 889
 890
 891
 892
 893
 894
 895
 896
 897
 898
 899
 900
 901
 902
 903
 904
 905
 906
 907
 908
 909
 910
 911
 912
 913
 914
 915
 916
 917
 918
 919
 920
 921
 922
 923
 924
 925
 926
 927
 928
 929
 930
 931
 932
 933
 934
 935
 936
 937
 938
 939
 940
 941
 942
 943
 944
 945
 946
 947
 948
 949
 950
 951
 952
 953
 954
 955
 956
 957
 958
 959
 960
 961
 962
 963
 964
 965
 966
 967
 968
 969
 970
 971
 972
 973
 974
 975
 976
 977
 978
 979
 980
 981
 982
 983
 984
 985
 986
 987
 988
 989
 990
 991
 992
 993
 994
 995
 996
 997
 998
 999
 1000



GenBank version 1.5
Copyright (c) 1994 - 2000 Nucleic Acid Research, Inc.

OM protein - protein search, using sw method

Run on: August 22, 2001, 14:25:57

Search time: 15.8 seconds
(with about 10.425 million on-line updates/sec)

File: us-08-659-254-8
Perfect score: 62
Sequence: 1 LNNQKWKKE 11

Scoring table:

BLAST2M62
Gapop: 10.0, Gapext: 0.5

Searched: 94435 seqs, 34253466 residues

Total number of hits satisfying chosen parameters: 9316

Minimum DB seq length: 0

Minimum DB seq length: 2000000000

Post-processing: Minimum Match: 0%

Maximum Match: 100%

Listing first 45 summaries

Database: SwissProt_391*

Pred. No. is the number of results provided by change to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the full score distribution.

SUMMARY

Result No.	Score	Query Match	Length	DB ID	Accession
1	62	100.0	284	1	STAR_MOUSE
2	62	100.0	284	1	STAR_MOUSE
3	57	91.9	284	1	STAR_MOUSE
4	57	91.9	284	1	STAR_MOUSE
5	57	91.9	284	1	STAR_MOUSE
6	57	91.9	284	1	STAR_MOUSE
7	51	82.3	285	1	STAR_MOUSE
8	43	69.4	157	1	STAR_MOUSE
9	40	64.5	620	1	STAR_MOUSE
10	40	64.5	1511	1	STAR_MOUSE
11	40	64.5	1529	1	STAR_MOUSE
12	39	62.9	1501	1	STAR_MOUSE
13	39	62.9	1742	1	STAR_MOUSE
14	38	61.3	451	1	STAR_MOUSE
15	38	61.3	475	1	STAR_MOUSE
16	38	61.3	1588	1	STAR_MOUSE
17	37	59.7	322	1	STAR_MOUSE
18	37	59.7	358	1	STAR_MOUSE
19	37	59.7	358	1	STAR_MOUSE
20	37	59.7	800	1	STAR_MOUSE
21	37	59.7	1271	1	STAR_MOUSE
22	36	58.1	114	1	STAR_MOUSE
23	36	58.1	134	1	STAR_MOUSE
24	36	58.1	330	1	STAR_MOUSE
25	36	58.1	453	1	STAR_MOUSE
26	36	58.1	458	1	STAR_MOUSE
27	36	58.1	458	1	STAR_MOUSE
28	36	58.1	505	1	STAR_MOUSE
29	36	58.1	799	1	STAR_MOUSE
30	36	58.1	865	1	STAR_MOUSE
31	36	58.1	877	1	STAR_MOUSE
32	36	58.1	887	1	STAR_MOUSE
33	36	58.1	887	1	STAR_MOUSE

34 35 50.5 269 1 DEM_MOUSE
35 35 50.5 280 1 DEM_MOUSE
36 35 50.5 411 1 DEM_MOUSE
37 35 50.5 493 1 DEM_MOUSE
38 35 50.5 406 1 DEM_MOUSE
39 35 50.5 417 1 DEM_MOUSE
40 35 50.5 420 1 DEM_MOUSE
41 35 50.5 439 1 DEM_MOUSE
42 35 50.5 446 1 DEM_MOUSE
43 35 50.5 489 1 DEM_MOUSE
44 35 50.5 489 1 DEM_MOUSE
45 35 50.5 563 1 DEM_MOUSE

ALL INFORMATION

RESULT 1
ID STAR_MOUSE
AC P51557
DT 01-OCT-1996 (Ver. 34, Created)
DT 01-OCT-1996 (Ver. 34, Last sequence update)
DT 30-MAY-2000 (Ver. 39, Last annotation update)
DE SPROLIDIC ACETATE KEMALATY PR-1 IN THE MESH-SPINNING MESH-RE-
DE INDUCED PROTEIN)
GN STAR_MOUSE
OS Mus musculus (mouse).
OC Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia; Muridae; Mus.
OX NCBI_TaxID 10090;
RN [1]
RP SEQUENCE FROM Y.A. AND PARTIAL SEQUENCE
RX MEDLINE 950444, PUBMED 764720
KA Clark R.J., Wells D., King S.R., et al. (1996) M.
KT "The putative protein, cloning, and expression of a novel putative
KT hormone-induced mitochondrial protein in MA to mouse Leydig tumor
KT cells. Characterization of the structure and function of the
KT (STAR) *
RL 1. Biol. Chem. 271:28314-28322 (1996)
CC 1. FUNCTION PLAYS A KEY ROLE IN THE HORMONE-INDUCED
CC ENHANCEMENT OF MITOCHONDRIAL PROTEIN SYNTHESIS
CC INADENOSINE TRIPHOSPHATE AND NUCLEOTIDE PHOSPHATE
CC INTERMEDIATE STAGE OF THE MITOCHONDRIAL (MIF) (MIF-1)
CC 2. SUBCELLULAR LOCATION: MITOCHONDRIA
CC 3. SIMILARITY: BELONGS TO THE STAR FAMILY
CC 4. This SWISS-Prot entry is copyright 1996, produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL partnership
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as it is credited to the source
CC modified and this statement is not removed, changed, or used for commercial
CC purposes. For more information, please contact the EMBL database at
CC or send an email to EMBL@EMBL.ch.
CC EMBL: L36062, AM94783, L36062
CC M30: M01:02760: Star
CC InterPro: IPR007994
CC InterPro: IPR007913
CC DR Pfam: PF01862: STAR1
CC DR PRINTS: PR00782: STARPROTEIN
CC KW Lipid binding, lipid transport, transport, storage, phospholipid
CC Mitochondrion, transport, peptide
CC TRANSIT 1
CC CHAIN 1
CC DOMAIN 178 174
CC STRESSES 264 666 47626 MW: 96694.21449072 707944
Query Match 100.0% Seq. Id. DB 12 Length 2844
Best Local Similarity 100.0% Pred. No. 9316
Matches 11, Identical 0, P-Value 0, Index 0, Maps 0

CC 1. SIMILARITY: BELONGS TO THE SWISS FAMILY

CC This SWISS-PROT entry is copyright. It is produced through a collaboration

CC between the Swiss Institute of Bioinformatics and the EMBL consortium.

CC The European Bioinformatics Institute. There are no restrictions on its

CC use by non-profit institutions as long as its content is in no way

CC modified and this statement is not removed, updated, or otherwise

CC or send an email to license@ebi.scrib.ac.uk

CC

DR EMBL: Y17259; CAA76717.1

DR EMBL: Y17260; CAA76718.1

DR InterPro: IPR000799; 1

DR InterPro: IPR002913; 1

DR Pfam: PF01852; STAFF-1

DR PROSITE: PS00598; STAFFPROTEIN

DR Lipid-binding: Lipid transport: Transport: Sterol lipoproteins

KM Mitochondrion: Transit peptide

FT TRANSLIT 1 285 MITOCHONDRION (PROTEIN)

FT CHAIN 2 285 STAFF PROTEIN (A) (K) (N) (M) (S) (E) (G) (H) (I) (L) (P) (Q) (R) (S) (T) (V) (W) (X) (Y) (Z) (AA) (AB) (AC) (AD) (AE) (AF) (AG) (AH) (AI) (AJ) (AK) (AL) (AM) (AN) (AO) (AP) (AQ) (AR) (AS) (AT) (AU) (AV) (AW) (AX) (AY) (AZ) (BA) (BB) (BC) (BD) (BE) (BF) (BG) (BH) (BI) (BJ) (BK) (BL) (BM) (BN) (BO) (BP) (BQ) (BR) (BS) (BT) (BU) (BV) (BW) (BX) (BY) (BZ) (CA) (CB) (CC) (CD) (CE) (CF) (CG) (CH) (CI) (CJ) (CK) (CL) (CM) (CN) (CO) (CP) (CQ) (CR) (CS) (CT) (CU) (CV) (CW) (CX) (CY) (CZ) (DA) (DB) (DC) (DD) (DE) (DF) (DG) (DH) (DI) (DJ) (DK) (DL) (DM) (DN) (DO) (DP) (DQ) (DR) (DS) (DT) (DU) (DV) (DW) (DX) (DY) (DZ) (EA) (EB) (EC) (ED) (EE) (EF) (EG) (EH) (EI) (EJ) (EK) (EL) (EM) (EN) (EO) (EP) (EQ) (ER) (ES) (ET) (EU) (EV) (EW) (EX) (EY) (EZ) (FA) (FB) (FC) (FD) (FE) (FF) (FG) (FH) (FI) (FJ) (FK) (FL) (FM) (FN) (FO) (FP) (FQ) (FR) (FS) (FT) (FU) (FV) (FW) (FX) (FY) (FZ) (GA) (GB) (GC) (GD) (GE) (GF) (GG) (GH) (GI) (GJ) (GK) (GL) (GM) (GN) (GO) (GP) (GQ) (GR) (GS) (GT) (GU) (GV) (GW) (GX) (GY) (GZ) (HA) (HB) (HC) (HD) (HE) (HF) (HG) (HH) (HI) (HJ) (HK) (HL) (HM) (HN) (HO) (HP) (HQ) (HR) (HS) (HT) (HU) (HV) (HW) (HX) (HY) (HZ) (IA) (IB) (IC) (ID) (IE) (IF) (IG) (IH) (II) (IJ) (IK) (IL) (IM) (IN) (IO) (IP) (IQ) (IR) (IS) (IT) (IU) (IV) (IW) (IX) (IY) (IZ) (JA) (JB) (JC) (JD) (JE) (JF) (JG) (JH) (JI) (JJ) (JK) (JL) (JM) (JN) (JO) (JP) (JQ) (JR) (JS) (JT) (JU) (JV) (JW) (JX) (JY) (JZ) (KA) (KB) (KC) (KD) (KE) (KF) (KG) (KH) (KI) (KJ) (KK) (KL) (KM) (KN) (KO) (KP) (KQ) (KR) (KS) (KT) (KU) (KV) (KW) (KX) (KY) (KZ) (LA) (LB) (LC) (LD) (LE) (LF) (LG) (LH) (LI) (LJ) (LK) (LL) (LM) (LN) (LO) (LP) (LQ) (LR) (LS) (LT) (LU) (LV) (LW) (LX) (LY) (LZ) (MA) (MB) (MC) (MD) (ME) (MF) (MG) (MH) (MI) (MJ) (MK) (ML) (MN) (MO) (MP) (MQ) (MR) (MS) (MT) (MU) (MV) (MW) (MX) (MY) (MZ) (NA) (NB) (NC) (ND) (NE) (NF) (NG) (NH) (NI) (NJ) (NK) (NL) (NM) (NO) (NP) (NQ) (NR) (NS) (NT) (NU) (NV) (NW) (NX) (NY) (NZ) (OA) (OB) (OC) (OD) (OE) (OF) (OG) (OH) (OI) (OJ) (OK) (OL) (OM) (ON) (OO) (OP) (OQ) (OR) (OS) (OT) (OU) (OV) (OW) (OX) (OY) (OZ) (PA) (PB) (PC) (PD) (PE) (PF) (PG) (PH) (PI) (PJ) (PK) (PL) (PM) (PN) (PO) (PP) (PQ) (PR) (PS) (PT) (PU) (PV) (PW) (PX) (PY) (PZ) (QA) (QB) (QC) (QD) (QE) (QF) (QG) (QH) (QI) (QJ) (QK) (QL) (QM) (QN) (QO) (QP) (QQ) (QR) (QS) (QT) (QU) (QV) (QW) (QX) (QY) (QZ) (RA) (RB) (RC) (RD) (RE) (RF) (RG) (RH) (RI) (RJ) (RK) (RL) (RM) (RN) (RO) (RP) (RQ) (RR) (RS) (RT) (RU) (RV) (RW) (RX) (RY) (RZ) (SA) (SB) (SC) (SD) (SE) (SF) (SG) (SH) (SI) (SJ) (SK) (SL) (SM) (SN) (SO) (SP) (SQ) (SR) (SS) (ST) (SU) (SV) (SW) (SX) (SY) (SZ) (TA) (TB) (TC) (TD) (TE) (TF) (TG) (TH) (TI) (TJ) (TK) (TL) (TM) (TN) (TO) (TP) (TQ) (TR) (TS) (TT) (TU) (TV) (TW) (TX) (TY) (TZ) (UA) (UB) (UC) (UD) (UE) (UF) (UG) (UH) (UI) (UJ) (UK) (UL) (UM) (UN) (UO) (UP) (UQ) (UR) (US) (UT) (UU) (UV) (UW) (UX) (UY) (UZ) (VA) (VB) (VC) (VD) (VE) (VF) (VG) (VH) (VI) (VJ) (VK) (VL) (VM) (VN) (VO) (VP) (VQ) (VR) (VS) (VT) (VU) (VV) (VW) (VX) (VY) (VZ) (WA) (WB) (WC) (WD) (WE) (WF) (WG) (WH) (WI) (WJ) (WK) (WL) (WM) (WN) (WO) (WP) (WQ) (WR) (WS) (WT) (WU) (WV) (WW) (WX) (WY) (WZ) (XA) (XB) (XC) (XD) (XE) (XF) (XG) (XH) (XI) (XJ) (XK) (XL) (XM) (XN) (XO) (XP) (XQ) (XR) (XS) (XT) (XU) (XV) (XW) (XX) (XY) (XZ) (YA) (YB) (YC) (YD) (YE) (YF) (YG) (YH) (YI) (YJ) (YK) (YL) (YM) (YN) (YO) (YP) (YQ) (YR) (YS) (YT) (YU) (YV) (YW) (YX) (YY) (YZ) (ZA) (ZB) (ZC) (ZD) (ZE) (ZF) (ZG) (ZH) (ZI) (ZJ) (ZK) (ZL) (ZM) (ZN) (ZO) (ZP) (ZQ) (ZR) (ZS) (ZT) (ZU) (ZV) (ZW) (ZX) (ZY) (ZZ)

Query Match 82.48; Score 51.0; Length 285

Best Local Similarity 81.88; Pred. No. 0.078

Matches 5; Conservative 1; Mismatch 0; Indels 0; Gaps 0

OY 1 LNNGBWKE 11

DB 89 LKQDEWKE 99

RESULT 8

DB3_SCHPO STANDARD: PRI 150 AA

AC P40984

DT 01-FEB-1995 (Rel. 41, created)

DT 01-FEB-1995 (Rel. 41, last sequence update)

DT 01-OCT-1996 (Rel. 44, last annotation update)

DE NUCLEOTIDE-DEPENDENT ENZYME (EC 3.1.1.1)

DE (00100111-PROTEIN 1165P H055) (00100111-PROTEIN 1165P H055)

DE (00100111-PROTEIN 1165P H055) (00100111-PROTEIN 1165P H055)

OS Schizosaccharomyces pombe (Fission yeast)

OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes

OC Schizosaccharomycetales; Schizosaccharomycetaceae

OC Schizosaccharomyces

OX NCBI_TaxID=4896

RN [1]

RE SEQUENCE FROM N.A.

RE MEDLINE=95286695; Pubmed=7768995

RE Al-Khodaly F., Enoch T., Haiman I.M., Jeff A.M.

RE "The Schizosaccharomyces pombe histone H4 encodes a ubiquitin

RE conjugating enzyme required for normal mitosis."

RE J. Cell Sci. 108:475-486(1995)

RK [2]

RN SEQUENCE FROM N.A.

RP STRAIN 97

RA Pearson D., Churcher G.M., Barto J.R., Fajardouan X.A., Walsh S.V.

RA Submitted (Nov-1995) to the EMBL/GenBank/DBJ databases

CC 1. FUNCTION: CATALYZES THE C-VALENT CATALYTIC DEGRADATION OF

CC OTHER PROTEINS. REQUIRED FOR EFFICIENT RECOVERY FROM DNA DAMAGE OF

CC S-PHASE ARREST AND NORMAL MITOSIS. THIS MAY BE AS PART OF A

CC CHECKPOINT INDEPENDENT RECOVERY PROCESS.

CC 2. CATALYTIC ACTIVITY: ATP + UBIQUITIN + PROTEIN LYSINE AMINO

CC PYROPHOSPHATE + PROTEIN N-UBIQUITIN CONJUGATE

CC 3. PATHWAY: SECOND STEP IN UBIQUITIN CONJUGATION.

CC 4. SUBCELLULAR LOCATION: NUCLEUS.

CC 5. MISCELLANEOUS: A CYSTEINE RESIDUE IS REQUIRED FOR

CC UBIQUITIN-THIOESTER FORMATION.

CC 6. SIMILARITY: BELONGS TO THE E1-RELATED NUCLEOTIDE-BINDING FAMILY

CC STRONGEST, TO YEAST UBC9.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration

CC between the Swiss Institute of Bioinformatics and the EMBL consortium.

CC The European Bioinformatics Institute. There are no restrictions on its

CC use by non-profit institutions as long as its content is in no way

CC modified and this statement is not removed, updated, or otherwise

CC or send an email to license@ebi.scrib.ac.uk

CC

DR EMBL: X81846; CAA57498.1

DR EMBL: Z67961; CAA91899.1

DR HSSP: P50550; YACS

DR InterPro: IPR003608

DR Pfam: PF00172; YACS

DR PROSITE: PS00183; UBIQUITIN-CONJUGATE

DR PROSITE: PS00183; UBIQUITIN-CONJUGATE

KM Ubiquitin conjugation: Ubiquitin-ubiquitin

KM Ubiquitin conjugation: Ubiquitin-ubiquitin

FT TRANSLIT 1 93

FT CHAIN 2 93

FT CONFLICT 75 93

FT CONFLICT 99 93

SEQUENCE 285 AA: EAFDSCALVSEZAS QKQVAT

Query Match 69.48; Score 6.0; Length 157

Best Local Similarity 77.88; Pred. No. 0.078

Matches 7; Conservative 1; Mismatch 0; Indels 0; Gaps 0

OY 1 LNNGBWKE 9

DB 96 LKQDEWKE 104

RESULT 9

Y018_YEAST STANDARD: PRI 92 AA

AC P51207

DT 01-OCT-1996 (Rel. 44, created)

DT 01-OCT-1996 (Rel. 44, last sequence update)

DT 01-NOV-1997 (Rel. 45, last annotation update)

DE HYDROLYTIC 71.4 KDa PROTEIN IN THE 9 MEM. MITOCHONDRIAL

DE YC0013W

OS Saccharomyces cerevisiae (Baker's yeast)

OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes

OC Saccharomycetales; Saccharomycetaceae; Saccharomyces

OC NCBI_TaxID=4932

RN [1]

RE SEQUENCE FROM N.A.

RE STRAIN: S288C

RE MEDLINE=9745481; Pubmed 929027

RE Kleger M., Hupfner M., Schaefer V., Mueller-Alto S.

RE "Sequence analysis of 202 kilobases of the Saccharomyces cerevisiae

RE chromosome VII."

RE Yeast 13:1077-1090(1997).

RK [2]

RN SEQUENCE FROM N.A.

RP STRAIN: S288C

RA Kleger M., Hupfner M., Schaefer V., Mueller-Alto S.

RA Submitted (Nov-1997) to the EMBL/GenBank/DBJ databases

CC 1. FUNCTION: CATALYZES THE C-VALENT CATALYTIC DEGRADATION OF

CC OTHER PROTEINS. REQUIRED FOR EFFICIENT RECOVERY FROM DNA DAMAGE OF

CC S-PHASE ARREST AND NORMAL MITOSIS. THIS MAY BE AS PART OF A

CC CHECKPOINT INDEPENDENT RECOVERY PROCESS.

CC 2. CATALYTIC ACTIVITY: ATP + UBIQUITIN + PROTEIN LYSINE AMINO

CC PYROPHOSPHATE + PROTEIN N-UBIQUITIN CONJUGATE

CC 3. PATHWAY: SECOND STEP IN UBIQUITIN CONJUGATION.

CC 4. SUBCELLULAR LOCATION: NUCLEUS.

CC 5. MISCELLANEOUS: A CYSTEINE RESIDUE IS REQUIRED FOR

CC UBIQUITIN-THIOESTER FORMATION.

CC 6. SIMILARITY: BELONGS TO THE E1-RELATED NUCLEOTIDE-BINDING FAMILY

CC STRONGEST, TO YEAST UBC9.

100001 10
 100002 10
 100003 10
 100004 10
 100005 10
 100006 10
 100007 10
 100008 10
 100009 10
 100010 10
 100011 10
 100012 10
 100013 10
 100014 10
 100015 10
 100016 10
 100017 10
 100018 10
 100019 10
 100020 10
 100021 10
 100022 10
 100023 10
 100024 10
 100025 10
 100026 10
 100027 10
 100028 10
 100029 10
 100030 10
 100031 10
 100032 10
 100033 10
 100034 10
 100035 10
 100036 10
 100037 10
 100038 10
 100039 10
 100040 10
 100041 10
 100042 10
 100043 10
 100044 10
 100045 10
 100046 10
 100047 10
 100048 10
 100049 10
 100050 10
 100051 10
 100052 10
 100053 10
 100054 10
 100055 10
 100056 10
 100057 10
 100058 10
 100059 10
 100060 10
 100061 10
 100062 10
 100063 10
 100064 10
 100065 10
 100066 10
 100067 10
 100068 10
 100069 10
 100070 10
 100071 10
 100072 10
 100073 10
 100074 10
 100075 10
 100076 10
 100077 10
 100078 10
 100079 10
 100080 10
 100081 10
 100082 10
 100083 10
 100084 10
 100085 10
 100086 10
 100087 10
 100088 10
 100089 10
 100090 10
 100091 10
 100092 10
 100093 10
 100094 10
 100095 10
 100096 10
 100097 10
 100098 10
 100099 10
 100100 10
 100101 10
 100102 10
 100103 10
 100104 10
 100105 10
 100106 10
 100107 10
 100108 10
 100109 10
 100110 10
 100111 10
 100112 10
 100113 10
 100114 10
 100115 10
 100116 10
 100117 10
 100118 10
 100119 10
 100120 10
 100121 10
 100122 10
 100123 10
 100124 10
 100125 10
 100126 10
 100127 10
 100128 10
 100129 10
 100130 10
 100131 10
 100132 10
 100133 10
 100134 10
 100135 10
 100136 10
 100137 10
 100138 10
 100139 10
 100140 10
 100141 10
 100142 10
 100143 10
 100144 10
 100145 10
 100146 10
 100147 10
 100148 10
 100149 10
 100150 10
 100151 10
 100152 10
 100153 10
 100154 10
 100155 10
 100156 10
 100157 10
 100158 10
 100159 10
 100160 10
 100161 10
 100162 10
 100163 10
 100164 10
 100165 10
 100166 10
 100167 10
 100168 10
 100169 10
 100170 10
 100171 10
 100172 10
 100173 10
 100174 10
 100175 10
 100176 10
 100177 10
 100178 10
 100179 10
 100180 10
 100181 10
 100182 10
 100183 10
 100184 10
 100185 10
 100186 10
 100187 10
 100188 10
 100189 10
 100190 10
 100191 10
 100192 10
 100193 10
 100194 10
 100195 10
 100196 10
 100197 10
 100198 10
 100199 10
 100200 10
 100201 10
 100202 10
 100203 10
 100204 10
 100205 10
 100206 10
 100207 10
 100208 10
 100209 10
 100210 10
 100211 10
 100212 10
 100213 10
 100214 10
 100215 10
 100216 10
 100217 10
 100218 10
 100219 10
 100220 10
 100221 10
 100222 10
 100223 10
 100224 10
 100225 10
 100226 10
 100227 10
 100228 10
 100229 10
 100230 10
 100231 10
 100232 10
 100233 10
 100234 10
 100235 10
 100236 10
 100237 10
 100238 10
 100239 10
 100240 10
 100241 10
 100242 10
 100243 10
 100244 10
 100245 10
 100246 10
 100247 10
 100248 10
 100249 10
 100250 10
 100251 10
 100252 10
 100253 10
 100254 10
 100255 10
 100256 10
 100257 10
 100258 10
 100259 10
 100260 10
 100261 10
 100262 10
 100263 10
 100264 10
 100265 10
 100266 10
 100267 10
 100268 10
 100269 10
 100270 10
 100271 10
 100272 10
 100273 10
 100274 10
 100275 10
 100276 10
 100277 10
 100278 10
 100279 10
 100280 10
 100281 10
 100282 10
 100283 10
 100284 10
 100285 10
 100286 10
 100287 10
 100288 10
 100289 10
 100290 10
 100291 10
 100292 10
 100

[illegible]

CC entries requires a license agreement. If you are not a licensee, please do not
 CC or send an email to license@slc.org.
 CC
 CC EMBL: U33274; AB04846.1;
 DR S50: S0002814; PDB15;
 DR InfoPro: 10P001617;
 DR Pfam: PF00005; ABC_TRAN_2;
 DR PROSITE: PS00211; ABC_TRANSPORTER_1;
 KW All-binding: Transmembrane; Glycoprotein; Transport;
 FT DOMAIN 1 531
 FT TRANSSEM 532 552
 FT TRANSSEM 568 588
 FT TRANSSEM 618 638
 FT TRANSSEM 643 663
 FT TRANSSEM 700 720
 FT TRANSSEM 784 804
 FT TRANSSEM 805 1219
 FT TRANSSEM 1223 1240
 FT TRANSSEM 1313 1333
 FT TRANSSEM 1341 1361
 FT TRANSSEM 1365 1389
 FT TRANSSEM 1397 1417
 FT TRANSSEM 1493 1513
 FT TRANSSEM 1514 1529
 FT TRANSSEM 1529 1544
 FT TRANSSEM 1544 1559
 FT TRANSSEM 1559 1574
 FT TRANSSEM 1574 1589
 FT TRANSSEM 1589 1604
 FT TRANSSEM 1604 1619
 FT TRANSSEM 1619 1634
 FT TRANSSEM 1634 1649
 FT TRANSSEM 1649 1664
 FT TRANSSEM 1664 1679
 FT TRANSSEM 1679 1694
 FT TRANSSEM 1694 1709
 FT TRANSSEM 1709 1724
 FT TRANSSEM 1724 1739
 FT TRANSSEM 1739 1754
 FT TRANSSEM 1754 1769
 FT TRANSSEM 1769 1784
 FT TRANSSEM 1784 1799
 FT TRANSSEM 1799 1814
 FT TRANSSEM 1814 1829
 FT TRANSSEM 1829 1844
 FT TRANSSEM 1844 1859
 FT TRANSSEM 1859 1874
 FT TRANSSEM 1874 1889
 FT TRANSSEM 1889 1904
 FT TRANSSEM 1904 1919
 FT TRANSSEM 1919 1934
 FT TRANSSEM 1934 1949
 FT TRANSSEM 1949 1964
 FT TRANSSEM 1964 1979
 FT TRANSSEM 1979 1994
 FT TRANSSEM 1994 2009
 FT TRANSSEM 2009 2024
 FT TRANSSEM 2024 2039
 FT TRANSSEM 2039 2054
 FT TRANSSEM 2054 2069
 FT TRANSSEM 2069 2084
 FT TRANSSEM 2084 2099
 FT TRANSSEM 2099 2114
 FT TRANSSEM 2114 2129
 FT TRANSSEM 2129 2144
 FT TRANSSEM 2144 2159
 FT TRANSSEM 2159 2174
 FT TRANSSEM 2174 2189
 FT TRANSSEM 2189 2204
 FT TRANSSEM 2204 2219
 FT TRANSSEM 2219 2234
 FT TRANSSEM 2234 2249
 FT TRANSSEM 2249 2264
 FT TRANSSEM 2264 2279
 FT TRANSSEM 2279 2294
 FT TRANSSEM 2294 2309
 FT TRANSSEM 2309 2324
 FT TRANSSEM 2324 2339
 FT TRANSSEM 2339 2354
 FT TRANSSEM 2354 2369
 FT TRANSSEM 2369 2384
 FT TRANSSEM 2384 2399
 FT TRANSSEM 2399 2414
 FT TRANSSEM 2414 2429
 FT TRANSSEM 2429 2444
 FT TRANSSEM 2444 2459
 FT TRANSSEM 2459 2474
 FT TRANSSEM 2474 2489
 FT TRANSSEM 2489 2504
 FT TRANSSEM 2504 2519
 FT TRANSSEM 2519 2534
 FT TRANSSEM 2534 2549
 FT TRANSSEM 2549 2564
 FT TRANSSEM 2564 2579
 FT TRANSSEM 2579 2594
 FT TRANSSEM 2594 2609
 FT TRANSSEM 2609 2624
 FT TRANSSEM 2624 2639
 FT TRANSSEM 2639 2654
 FT TRANSSEM 2654 2669
 FT TRANSSEM 2669 2684
 FT TRANSSEM 2684 2699
 FT TRANSSEM 2699 2714
 FT TRANSSEM 2714 2729
 FT TRANSSEM 2729 2744
 FT TRANSSEM 2744 2759
 FT TRANSSEM 2759 2774
 FT TRANSSEM 2774 2789
 FT TRANSSEM 2789 2804
 FT TRANSSEM 2804 2819
 FT TRANSSEM 2819 2834
 FT TRANSSEM 2834 2849
 FT TRANSSEM 2849 2864
 FT TRANSSEM 2864 2879
 FT TRANSSEM 2879 2894
 FT TRANSSEM 2894 2909
 FT TRANSSEM 2909 2924
 FT TRANSSEM 2924 2939
 FT TRANSSEM 2939 2954
 FT TRANSSEM 2954 2969
 FT TRANSSEM 2969 2984
 FT TRANSSEM 2984 2999
 FT TRANSSEM 2999 3014
 FT TRANSSEM 3014 3029
 FT TRANSSEM 3029 3044
 FT TRANSSEM 3044 3059
 FT TRANSSEM 3059 3074
 FT TRANSSEM 3074 3089
 FT TRANSSEM 3089 3104
 FT TRANSSEM 3104 3119
 FT TRANSSEM 3119 3134
 FT TRANSSEM 3134 3149
 FT TRANSSEM 3149 3164
 FT TRANSSEM 3164 3179
 FT TRANSSEM 3179 3194
 FT TRANSSEM 3194 3209
 FT TRANSSEM 3209 3224
 FT TRANSSEM 3224 3239
 FT TRANSSEM 3239 3254
 FT TRANSSEM 3254 3269
 FT TRANSSEM 3269 3284
 FT TRANSSEM 3284 3299
 FT TRANSSEM 3299 3314
 FT TRANSSEM 3314 3329
 FT TRANSSEM 3329 3344
 FT TRANSSEM 3344 3359
 FT TRANSSEM 3359 3374
 FT TRANSSEM 3374 3389
 FT TRANSSEM 3389 3404
 FT TRANSSEM 3404 3419
 FT TRANSSEM 3419 3434
 FT TRANSSEM 3434 3449
 FT TRANSSEM 3449 3464
 FT TRANSSEM 3464 3479
 FT TRANSSEM 3479 3494
 FT TRANSSEM 3494 3509
 FT TRANSSEM 3509 3524
 FT TRANSSEM 3524 3539
 FT TRANSSEM 3539 3554
 FT TRANSSEM 3554 3569
 FT TRANSSEM 3569 3584
 FT TRANSSEM 3584 3599
 FT TRANSSEM 3599 3614
 FT TRANSSEM 3614 3629
 FT TRANSSEM 3629 3644
 FT TRANSSEM 3644 3659
 FT TRANSSEM 3659 3674
 FT TRANSSEM 3674 3689
 FT TRANSSEM 3689 3704
 FT TRANSSEM 3704 3719
 FT TRANSSEM 3719 3734
 FT TRANSSEM 3734 3749
 FT TRANSSEM 3749 3764
 FT TRANSSEM 3764 3779
 FT TRANSSEM 3779 3794
 FT TRANSSEM 3794 3809
 FT TRANSSEM 3809 3824
 FT TRANSSEM 3824 3839
 FT TRANSSEM 3839 3854
 FT TRANSSEM 3854 3869
 FT TRANSSEM 3869 3884
 FT TRANSSEM 3884 3899
 FT TRANSSEM 3899 3914
 FT TRANSSEM 3914 3929
 FT TRANSSEM 3929 3944
 FT TRANSSEM 3944 3959
 FT TRANSSEM 3959 3974
 FT TRANSSEM 3974 3989
 FT TRANSSEM 3989 4004
 FT TRANSSEM 4004 4019
 FT TRANSSEM 4019 4034
 FT TRANSSEM 4034 4049
 FT TRANSSEM 4049 4064
 FT TRANSSEM 4064 4079
 FT TRANSSEM 4079 4094
 FT TRANSSEM 4094 4109
 FT TRANSSEM 4109 4124
 FT TRANSSEM 4124 4139
 FT TRANSSEM 4139 4154
 FT TRANSSEM 4154 4169
 FT TRANSSEM 4169 4184
 FT TRANSSEM 4184 4199
 FT TRANSSEM 4199 4214
 FT TRANSSEM 4214 4229
 FT TRANSSEM 4229 4244
 FT TRANSSEM 4244 4259
 FT TRANSSEM 4259 4274
 FT TRANSSEM 4274 4289
 FT TRANSSEM 4289 4304
 FT TRANSSEM 4304 4319
 FT TRANSSEM 4319 4334
 FT TRANSSEM 4334 4349
 FT TRANSSEM 4349 4364
 FT TRANSSEM 4364 4379
 FT TRANSSEM 4379 4394
 FT TRANSSEM 4394 4409
 FT TRANSSEM 4409 4424
 FT TRANSSEM 4424 4439
 FT TRANSSEM 4439 4454
 FT TRANSSEM 4454 4469
 FT TRANSSEM 4469 4484
 FT TRANSSEM 4484 4499
 FT TRANSSEM 4499 4514
 FT TRANSSEM 4514 4529
 FT TRANSSEM 4529 4544
 FT TRANSSEM 4544 4559
 FT TRANSSEM 4559 4574
 FT TRANSSEM 4574 4589
 FT TRANSSEM 4589 4604
 FT TRANSSEM 4604 4619
 FT TRANSSEM 4619 4634
 FT TRANSSEM 4634 4649
 FT TRANSSEM 4649 4664
 FT TRANSSEM 4664 4679
 FT TRANSSEM 4679 4694
 FT TRANSSEM 4694 4709
 FT TRANSSEM 4709 4724
 FT TRANSSEM 4724 4739
 FT TRANSSEM 4739 4754
 FT TRANSSEM 4754 4769
 FT TRANSSEM 4769 4784
 FT TRANSSEM 4784 4799
 FT TRANSSEM 4799 4814
 FT TRANSSEM 4814 4829
 FT TRANSSEM 4829 4844
 FT TRANSSEM 4844 4859
 FT TRANSSEM 4859 4874
 FT TRANSSEM 4874 4889
 FT TRANSSEM 4889 4904
 FT TRANSSEM 4904 4919
 FT TRANSSEM 4919 4934
 FT TRANSSEM 4934 4949
 FT TRANSSEM 4949 4964
 FT TRANSSEM 4964 4979
 FT TRANSSEM 4979 4994
 FT TRANSSEM 4994 5009
 FT TRANSSEM 5009 5024
 FT TRANSSEM 5024 5039
 FT TRANSSEM 5039 5054
 FT TRANSSEM 5054 5069
 FT TRANSSEM 5069 5084
 FT TRANSSEM 5084 5099
 FT TRANSSEM 5099 5114
 FT TRANSSEM 5114 5129
 FT TRANSSEM 5129 5144
 FT TRANSSEM 5144 5159
 FT TRANSSEM 5159 5174
 FT TRANSSEM 5174 5189
 FT TRANSSEM 5189 5204
 FT TRANSSEM 5204 5219
 FT TRANSSEM 5219 5234
 FT TRANSSEM 5234 5249
 FT TRANSSEM 5249 5264
 FT TRANSSEM 5264 5279
 FT TRANSSEM 5279 5294
 FT TRANSSEM 5294 5309
 FT TRANSSEM 5309 5324
 FT TRANSSEM 5324 5339
 FT TRANSSEM 5339 5354
 FT TRANSSEM 5354 5369
 FT TRANSSEM 5369 5384
 FT TRANSSEM 5384 5399
 FT TRANSSEM 5399 5414
 FT TRANSSEM 5414 5429
 FT TRANSSEM 5429 5444
 FT TRANSSEM 5444 5459
 FT TRANSSEM 5459 5474
 FT TRANSSEM 5474 5489
 FT TRANSSEM 5489 5504
 FT TRANSSEM 5504 5519
 FT TRANSSEM 5519 5534
 FT TRANSSEM 5534 5549
 FT TRANSSEM 5549 5564
 FT TRANSSEM 5564 5579
 FT TRANSSEM 5579 5594
 FT TRANSSEM 5594 5609
 FT TRANSSEM 5609 5624
 FT TRANSSEM 5624 5639
 FT TRANSSEM 5639 5654
 FT TRANSSEM 5654 5669
 FT TRANSSEM 5669 5684
 FT TRANSSEM 5684 5699
 FT TRANSSEM 5699 5714
 FT TRANSSEM 5714 5729
 FT TRANSSEM 5729 5744
 FT TRANSSEM 5744 5759
 FT TRANSSEM 5759 5774
 FT TRANSSEM 5774 5789
 FT TRANSSEM 5789 5804
 FT TRANSSEM 5804 5819
 FT TRANSSEM 5819 5834
 FT TRANSSEM 5834 5849
 FT TRANSSEM 5849 5864
 FT TRANSSEM 5864 5879
 FT TRANSSEM 5879 5894
 FT TRANSSEM 5894 5909
 FT TRANSSEM 5909 5924
 FT TRANSSEM 5924 5939
 FT TRANSSEM 5939 5954
 FT TRANSSEM 5954 5969
 FT TRANSSEM 5969 5984
 FT TRANSSEM 5984 5999
 FT TRANSSEM 5999 6014
 FT TRANSSEM 6014 6029
 FT TRANSSEM 6029 6044
 FT TRANSSEM 6044 6059
 FT TRANSSEM 6059 6074
 FT TRANSSEM 6074 6089
 FT TRANSSEM 6089 6104
 FT TRANSSEM 6104 6119
 FT TRANSSEM 6119 6134
 FT TRANSSEM 6134 6149
 FT TRANSSEM 6149 6164
 FT TRANSSEM 6164 6179
 FT TRANSSEM 6179 6194
 FT TRANSSEM 6194 6209
 FT TRANSSEM 6209 6224
 FT TRANSSEM 6224 6239
 FT TRANSSEM 6239 6254
 FT TRANSSEM 6254 6269
 FT TRANSSEM 6269 6284
 FT TRANSSEM 6284 6299
 FT TRANSSEM 6299 6314
 FT TRANSSEM 6314 6329
 FT TRANSSEM 6329 6344
 FT TRANSSEM 6344 6359
 FT TRANSSEM 6359 6374
 FT TRANSSEM 6374 6389
 FT TRANSSEM 6389 6404
 FT TRANSSEM 6404 6419
 FT TRANSSEM 6419 6434
 FT TRANSSEM 6434 6449
 FT TRANSSEM 6449 6464
 FT TRANSSEM 6464 6479
 FT TRANSSEM 6479 6494
 FT TRANSSEM 6494 6509
 FT TRANSSEM 6509 6524
 FT TRANSSEM 6524 6539
 FT TRANSSEM 6539 6554
 FT TRANSSEM 6554 6569
 FT TRANSSEM 6569 6584
 FT TRANSSEM 6584 6599
 FT TRANSSEM 6599 6614
 FT TRANSSEM 6614 6629
 FT TRANSSEM 6629 6644
 FT TRANSSEM 6644 6659
 FT TRANSSEM 6659 6674
 FT TRANSSEM 6674 6689
 FT TRANSSEM 6689 6704
 FT TRANSSEM 6704 6719
 FT TRANSSEM 6719 6734
 FT TRANSSEM 6734 6749
 FT TRANSSEM 6749 6764
 FT TRANSSEM 6764 6779
 FT TRANSSEM 6779 6794
 FT TRANSSEM 6794 6809
 FT TRANSSEM 6809 6824
 FT TRANSSEM 6824 6839
 FT TRANSSEM 6839 6854
 FT TRANSSEM 6854 6869
 FT TRANSSEM 6869 6884
 FT TRANSSEM 6884 6899
 FT TRANSSEM 6899 6914
 FT TRANSSEM 6914 6929
 FT TRANSSEM 6929 6944
 FT TRANSSEM 6944 6959
 FT TRANSSEM 6959 6974
 FT TRANSSEM 6974 6989
 FT TRANSSEM 6989 7004
 FT TRANSSEM 7004 7019
 FT TRANSSEM 7019 7034
 FT TRANSSEM 7034 7049
 FT TRANSSEM 7049 7064
 FT TRANSSEM 7064 7079
 FT TRANSSEM 7079 7094
 FT TRANSSEM 7094 7109
 FT TRANSSEM 7109 7124
 FT TRANSSEM 7124 7139
 FT TRANSSEM 7139 7154
 FT TRANSSEM 7154 7169
 FT TRANSSEM 7169 7184
 FT TRANSSEM 7184 7199
 FT TRANSSEM 7199 7214
 FT TRANSSEM 7214 7229
 FT TRANSSEM 7229 7244
 FT TRANSSEM 7244 7259
 FT TRANSSEM 7259 7274
 FT TRANSSEM 7274 7289
 FT TRANSSEM 7289 7304
 FT TRANSSEM 7304 7319
 FT TRANSSEM 7319 7334
 FT TRANSSEM 7334 7349
 FT TRANSSEM 7349 7364
 FT TRANSSEM 7364 7379
 FT TRANSSEM 7379 7394
 FT TRANSSEM 7394 7409
 FT TRANSSEM 7409 7424
 FT TRANSSEM 7424 7439
 FT TRANSSEM 7439 7454
 FT TRANSSEM 7454 7469
 FT TRANSSEM 7469 7484
 FT TRANSSEM 7484 7499
 FT TRANSSEM 7499 7514
 FT TRANSSEM 7514 7529
 FT TRANSSEM 7529 7544
 FT TRANSSEM 7544 7559
 FT TRANSSEM 7559 7574
 FT TRANSSEM 7574 7589
 FT TRANSSEM 7589 7604
 FT TRANSSEM 7604 7619
 FT TRANSSEM 7619 7634
 FT TRANSSEM 7634 7649
 FT TRANSSEM 7649 7664
 FT TRANSSEM 7664 7679
 FT TRANSSEM 7679 7694
 FT TRANSSEM 7694 7709
 FT TRANSSEM 7709 7724
 FT TRANSSEM 7724 7739
 FT TRANSSEM 7739 7754
 FT TRANSSEM 7754 7769
 FT TRANSSEM 7769 7784
 FT TRANSSEM 7784 7799
 FT TRANSSEM 7799 7814
 FT TRANSSEM 7814 7829
 FT TRANSSEM 7829 7844
 FT TRANSSEM 7844 7859
 FT TRANSSEM 7859 7874
 FT TRANSSEM 7874 7889
 FT TRANSSEM 7889 7904
 FT TRANSSEM 7904 7919
 FT TRANSSEM 7919 7934
 FT TRANSSEM 7934 7949
 FT TRANSSEM 7949 7964
 FT TRANSSEM 7964 7979
 FT TRANSSEM 7979 7994
 FT TRANSSEM 7994 8009
 FT TRANSSEM 8009 8024
 FT TRANSSEM 8024 8039
 FT TRANSSEM 8039 8054
 FT TRANSSEM 8054 8069
 FT TRANSSEM 8069 8084
 FT TRANSSEM 8084 8099
 FT TRANSSEM 8099 8114
 FT TRANSSEM 8114 8129
 FT TRANSSEM 8129 8144
 FT TRANSSEM 8144 8159
 FT TRANSSEM 8159 8174
 FT TRANSSEM 8174 8189
 FT TRANSSEM 8189 8204
 FT TRANSSEM 8204 8219
 FT TRANSSEM 8219 8234
 FT TRANSSEM 8234 8249
 FT TRANSSEM 8249 8264
 FT TRANSSEM 8264 8279
 FT TRANSSEM 8279 8294
 FT TRANSSEM 8294 8309
 FT TRANSSEM 8309 8324
 FT TRANSSEM 8324 8339
 FT TRANSSEM 8339 8354
 FT TRANSSEM 8354 8369
 FT TRANSSEM 8369 8384
 FT TRANSSEM 8384 8399
 FT TRANSSEM 8399 8414
 FT TRANSSEM 8414 8429
 FT TRANSSEM 8429 8444
 FT TRANSSEM 8444 8459
 FT TRANSSEM 8459 8474
 FT TRANSSEM 8474 8489
 FT TRANSSEM 8489 8504
 FT TRANSSEM 8504 8519
 FT TRANSSEM 8519 8534
 FT TRANSSEM 8534 8549
 FT TRANSSEM 8549 8564
 FT TRANSSEM 8564 8579
 FT TRANSSEM 8579 8594
 FT TRANSSEM 8594 8609
 FT TRANSSEM 8609 8624
 FT TRANSSEM 8624 8639
 FT TRANSSEM 8639 8654
 FT TRANSSEM 8654 8669
 FT TRANSSEM 8669 8684
 FT TRANSSEM 8684 8699
 FT TRANSSEM 8699 8714
 FT TRANSSEM 8714 8729
 FT TRANSSEM 8729 8744
 FT TRANSSEM 8744 8759
 FT TRANSSEM 8759 8774
 FT TRANSSEM 8774 8789
 FT TRANSSEM 8789 8804
 FT TRANSSEM 8804 8819
 FT TRANSSEM 8819 8834
 FT TRANSSEM 8834 8849
 FT TRANSSEM 8849 8864
 FT TRANSSEM 8864 8879
 FT TRANSSEM 8879 8894
 FT TRANSSEM 8894 8909
 FT TRANSSEM 8909 8924
 FT TRANSSEM 8924 8939
 FT TRANSSEM 8939 8954
 FT TRANSSEM 8954 8969
 FT TRANSSEM 8969 8984
 FT TRANSSEM 8984 8999
 FT TRANSSEM 8999 9014
 FT TRANSSEM 9014 9029
 FT TRANSSEM 9029 9044
 FT TRANSSEM 9044 9059
 FT TRANSSEM 9059 9074
 FT TRANSSEM 9074 9089
 FT TRANSSEM 9089 9104
 FT TRANSSEM 9104 9119
 FT TRANSSEM 9119 9134
 FT TRANSSEM 9134 9149
 FT TRANSSEM 9149 9164
 FT TRANSSEM 9164 9179
 FT TRANSSEM 9179 9194
 FT TRANSSEM 9194 9209
 FT TRANSSEM 9209 9224
 FT TRANSSEM 9224 9239
 FT TRANSSEM 9239 9254
 FT TRANSSEM 9254 9269
 FT TRANSSEM 9269 9284
 FT TRANSSEM 9284 9299
 FT TRANSSEM 9299 9314
 FT TRANSSEM 9314 9329
 FT TRANSSEM 9329 9344
 FT TRANSSEM 9344 9359
 FT TRANSSEM 9359 9374
 FT TRANSSEM 9374 9389
 FT TRANSSEM 9389 9404
 FT TRANSSEM 9404 9419
 FT TRANSSEM 9419 9434
 FT TRANSSEM 9434 9449
 FT TRANSSEM 9449 9464
 FT TRANSSEM 9464 9479
 FT TRANSSEM 9479 9494
 FT TRANSSEM 9494 9509
 FT TRANSSEM 9509 9524
 FT TRANSSEM 9524 9539
 FT TRANSSEM 9539 9554
 FT TRANSSEM 9554 9569
 FT TRANSSEM 9569 9584
 FT TRANSSEM 9584 9599
 FT TRANSSEM 9599 9614
 FT TRANSSEM 9614 9629
 FT TRANSSEM 9629 9644
 FT TRANSSEM 9644 9659
 FT TRANSSEM 9659 9674
 FT TRANSSEM 9674 9689
 FT TRANSSEM 9689 9704
 FT TRANSSEM 9704 9719
 FT TRANSSEM 9719 9734
 FT TRANSSEM 9734 9749
 FT TRANSSEM 9749 9764
 FT TRANSSEM 9764 9779
 FT TRANSSEM 9779 9794
 FT TRANSSEM 9794 9809
 FT TRANSSEM 9809 9824
 FT TRANSSEM 9824 9839
 FT TRANSSEM 9839 9854
 FT TRANSSEM 9854 9869
 FT TRANSSEM 9869 9884
 FT TRANSSEM 9884 9899
 FT TRANSSEM 9899 9914
 FT TRANSSEM 9914 9929
 FT TRANSSEM 9929 9944
 FT TRANSSEM 9944 9959
 FT TRANSSEM 9959 9974
 FT TRANSSEM 9974 9989
 FT TRANSSEM 9989 10000
 FT TRANSSEM 10000 10014
 FT TRANSSEM 10014 10029
 FT TRANSSEM 10029 10044
 FT TRANSSEM 10044 10059
 FT TRANSSEM 10059 10074
 FT TRANSSEM 10074 10089
 FT TRANSSEM 10089 10104
 FT TRANSSEM 10104 10119
 FT TRANSSEM 10119 10134
 FT TRANSSEM 10134 10149
 FT TRANSSEM 10149 10164
 FT TRANSSEM 10164 10179
 FT TRANSSEM 10179 10194
 FT TRANSSEM 10194 10209
 FT TRANSSEM 10209 10224
 FT TRANSSEM 10224 10239
 FT TRANSSEM 10239 10254
 FT TRANSSEM 10254 10269
 FT TRANSSEM 10269 10284
 FT TRANSSEM 10284 10299
 FT TRANSSEM 10299 10314
 FT TRANSSEM 10314 10329
 FT TRANSSEM 10329 10344
 FT TRANSSEM 10344 10359
 FT TRANSSEM 10359 10374
 FT TRANSSEM 10374 10389
 FT TRANSSEM 10389 10404
 FT TRANSSEM 10404 10419
 FT TRANSSEM 10419 10434
 FT TRANSSEM 10434 10449
 FT TRANSSEM 10449 10464
 FT TRANSSEM 10464 10479
 FT TRANSSEM 10479 10494
 FT TRANSSEM 10494 10509
 FT TRANSSEM 10509 10524
 FT TRANSSEM 10524 10539
 FT TRANSSEM 10539 10554
 FT TRANSSEM 10554 10569
 FT TRANSSEM 10569 10584
 FT TRANSSEM 10584 10599
 FT TRANSSEM 10599 10614
 FT TRANSSEM 10614 10629
 FT TRANSSEM 10629 10644
 FT TRANSSEM 10644 10659
 FT TRANSSEM 10659 10674
 FT TRANSSEM 10674 10689
 FT TRANSSEM 10689 10704
 FT TRANSSEM 10704 10719
 FT TRANSSEM 10719 10734
 FT TRANSSEM 10734 10749
 FT TRANSSEM 10749 10764
 FT TRANSSEM 10764 10779
 FT TRANSSEM 10779 10794
 FT TRANSSEM 10794 10809
 FT TRANSSEM 10809 10824
 FT TRANSSEM 10824 10839
 FT TRANSSEM 10839 10854
 FT TRANSSEM 10854 10869
 FT TRANSSEM 10869 10884
 FT TRANSSEM 10884 10899
 FT TRANSSEM 10899 10914
 FT TRANSSEM 10914 10929
 FT TRANSSEM 10929 10944
 FT TRANSSEM 10944 10959
 FT TRANSSEM 10959 10974
 FT TRANSSEM 10974 10989
 FT TRANSSEM 10989 11000
 FT TRANSSEM 11000 11014
 FT TRANSSEM 11014 11029
 FT TRANSSEM 11029 11044
 FT TRANSSEM 11044 11059
 FT TRANSSEM 11059 11074
 FT TRANSSEM 11074 11089
 FT TRANSSEM 11089 11104
 FT TRANSSEM 11104 11119
 FT TRANSSEM 11119 11134
 FT TRANSSEM 11134 11149
 FT TRANSSEM 11149 11164
 FT TRANSSEM 11164 11179
 FT TRANSSEM 11179 11194
 FT TRANSSEM 11194 11209
 FT TRANSSEM 11209 11224
 FT TRANSSEM 11224 11239
 FT TRANSSEM 11239 11254
 FT TRANSSEM 11254 11269
 FT TRANSSEM 11269 11284
 FT TRANSSEM 11284 11299
 FT TRANSSEM 11299 11314
 FT TRANSSEM 11314 11329
 FT TRANSSEM 11329 11344
 FT TRANSSEM 11344 11359
 FT TRANSSEM 11359 11374
 FT TRANSSEM 11374 11389
 FT TRANSSEM 11389 11404
 FT TRANSSEM 11404 11419
 FT TRANSSEM 11419 11434
 FT TRANSSEM 11434 11449
 FT TRANSSEM 11449 11464
 FT TRANSSEM 11464 11479
 FT TRANSSEM 11479 11494
 FT TRANSSEM 11494 11509
 FT TRANSSEM 11509 11524
 FT TRANSSEM 11524 11539
 FT TRANSSEM 11539 11554
 FT TRANSSEM 11554 11569
 FT TRANSSEM 11569 11584
 FT TRANSSEM 11584 11599
 FT TRANSSEM 11599 11614
 FT TRANSSEM 11614 11629
 FT TRANSSEM 11629 11644
 FT TRANSSEM 11644 11659
 FT TRANSSEM 11659 11674
 FT TRANSSEM 11674 11689
 FT TRANSSEM 11689 11704
 FT TRANSSEM 11704 11719
 FT TRANSSEM 11719 11734
 FT TRANSSEM 117

CC This SWISS-PROI entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation
 CC the European Bioinformatics Institute. These are not responsible for
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed, altered, by any means
 CC or send an email to licensing@ebi.ac.uk or
 CC or send an email to licensing@ebi.ac.uk
 CC
 CC EMBL: AP20144; AAF09585.1; -
 CC KW Microtubules; GTP-binding; GTP (GTPase);
 CC FT NP_BIND 148 154
 CC SQ SEQUENCE 475 AA; 52941 MW; 3484717.050/AF09585.1/004;

Query Match 61.48; Score 44; e-1; Length 175;
 Best Local Similarity 100.0%; Pos. No. 1;
 Matches 6; Conservative 0; Mismatch 0; Indels 0; Gaps 0

QY 4 NQRCWK 9
 DB 476 NQRCWK 481

Search completed: August 22, 2001, 14:43:04
 Job time: 412 sec



GenInfo version 1.5
Copyright (c) 1993 - 2000 Empress Ltd.

OM protein - protein search, using sw mod 1

Run on: August 22, 2001, 14:27:25

Search time: 11:12:00
(2.080 Million cell updates/sec)

Title: US-08-659-254 8

Perfect score: 62

Sequence: 1:LNNGBWRKE:11

Scoring table: BLAST62

Gapop: 10.0, Gapext: 0.0

Searched: 42502 seqs, 13279527 residues

Total number of hits satisfying chosen parameters: 42502

num DB seq length: 0

num DB seq length: 200900000

Post-processing: Minimum Match: 0.8

Maximum Match: 100%

Listing first 45 summaries

Database: 1: SP archaea: 2: SP bacteria: 3: SP fungi: 4: SP human: 5: SP invertebrate: 6: SP mammal: 7: SP mhc: 8: SP organelle: 9: SP phage: 10: SP plant: 11: SP rodent: 12: SP unclassified: 13: SP vertebrate: 14: SP virus:

Prod. No. is the number of results identified by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the score distribution.

SUMMARYS

Hit no.	Score	Query Match	Length	ID	Description
1	51	82.3	285	6	Q9GMD0
2	45	72.6	281	13	Q9GMD0
3	42	67.7	284	13	Q9GMD0
4	42	67.7	783	2	Q45564
5	41	66.1	800	1	Q59066
6	40	64.5	704	3	Q9P811
7	40	64.5	1499	3	Q9UVV5
8	40	64.5	1542	3	Q91258
9	39	62.9	1022	11	Q9P720
10	39	62.9	1022	11	Q9P720
11	39	62.9	1022	11	Q9P720
12	39	62.9	1022	11	Q9P720
13	39	62.9	1022	11	Q9P720
14	39	62.9	1022	11	Q9P720
15	39	62.9	1022	11	Q9P720
16	38	61.3	95	5	Q9VW89
17	38	61.3	117	10	Q9S778
18	38	61.3	119	5	Q45647
19	38	61.3	226	2	Q9XW07

20	38	61.3	285	13	Q9GMD0
21	38	61.3	403	11	Q9GMD0
22	38	61.3	416	4	Q9VW89
23	38	61.3	460	4	Q9VW89
24	38	61.3	460	4	Q9VW89
25	38	61.3	460	4	Q9VW89
26	38	61.3	460	4	Q9VW89
27	38	61.3	460	4	Q9VW89
28	38	61.3	460	4	Q9VW89
29	38	61.3	460	4	Q9VW89
30	38	61.3	460	4	Q9VW89
31	38	61.3	460	4	Q9VW89
32	38	61.3	460	4	Q9VW89
33	38	61.3	460	4	Q9VW89
34	38	61.3	460	4	Q9VW89
35	38	61.3	460	4	Q9VW89
36	38	61.3	460	4	Q9VW89
37	38	61.3	460	4	Q9VW89
38	38	61.3	460	4	Q9VW89
39	38	61.3	460	4	Q9VW89
40	38	61.3	460	4	Q9VW89
41	38	61.3	460	4	Q9VW89
42	38	61.3	460	4	Q9VW89
43	38	61.3	460	4	Q9VW89
44	38	61.3	460	4	Q9VW89
45	38	61.3	460	4	Q9VW89

ALL HITS

RESULT	ID	DESCRIPTION	Prod. No.	Score	Query Match	Length	ID	Description
1	Q9GMD0	PRELIMINARY: 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45	285	AA	82.3	285	6	Q9GMD0
2	Q9GMD0	PRELIMINARY: 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45	285	AA	72.6	281	13	Q9GMD0
3	Q9GMD0	PRELIMINARY: 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45	285	AA	67.7	284	13	Q9GMD0
4	Q9GMD0	PRELIMINARY: 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45	285	AA	67.7	783	2	Q45564
5	Q9GMD0	PRELIMINARY: 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45	285	AA	66.1	800	1	Q59066
6	Q9GMD0	PRELIMINARY: 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45	285	AA	64.5	704	3	Q9P811
7	Q9GMD0	PRELIMINARY: 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45	285	AA	64.5	1499	3	Q9UVV5
8	Q9GMD0	PRELIMINARY: 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45	285	AA	64.5	1542	3	Q91258
9	Q9GMD0	PRELIMINARY: 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45	285	AA	62.9	1022	11	Q9P720
10	Q9GMD0	PRELIMINARY: 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45	285	AA	62.9	1022	11	Q9P720
11	Q9GMD0	PRELIMINARY: 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45	285	AA	62.9	1022	11	Q9P720
12	Q9GMD0	PRELIMINARY: 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45	285	AA	62.9	1022	11	Q9P720
13	Q9GMD0	PRELIMINARY: 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45	285	AA	62.9	1022	11	Q9P720
14	Q9GMD0	PRELIMINARY: 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45	285	AA	62.9	1022	11	Q9P720
15	Q9GMD0	PRELIMINARY: 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45	285	AA	62.9	1022	11	Q9P720
16	Q9GMD0	PRELIMINARY: 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45	285	AA	61.3	95	5	Q9VW89
17	Q9GMD0	PRELIMINARY: 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45	285	AA	61.3	117	10	Q9S778
18	Q9GMD0	PRELIMINARY: 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45	285	AA	61.3	119	5	Q45647
19	Q9GMD0	PRELIMINARY: 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45	285	AA	61.3	226	2	Q9XW07

Query Match	Best Local Similarity	Prod. No.	Score	Query Match	Length	ID	Description
2	82.3	AA	285	6	Q9GMD0	Q9GMD0	PRELIMINARY: 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45
1	72.6	AA	281	13	Q9GMD0	Q9GMD0	PRELIMINARY: 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45
1	67.7	AA	284	13	Q9GMD0	Q9GMD0	PRELIMINARY: 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45
2	67.7	AA	783	2	Q45564	Q45564	PRELIMINARY: 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45
1	66.1	AA	800	1	Q59066	Q59066	PRELIMINARY: 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45
3	64.5	AA	704	3	Q9P811	Q9P811	PRELIMINARY: 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45
3	64.5	AA	1499	3	Q9UVV5	Q9UVV5	PRELIMINARY: 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45
3	64.5	AA	1542	3	Q91258	Q91258	PRELIMINARY: 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45
11	62.9	AA	1022	11	Q9P720	Q9P720	PRELIMINARY: 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45
11	62.9	AA	1022	11	Q9P720	Q9P720	PRELIMINARY: 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45
11	62.9	AA	1022	11	Q9P720	Q9P720	PRELIMINARY: 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45
11	62.9	AA	1022	11	Q9P720	Q9P720	PRELIMINARY: 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45
5	61.3	AA	95	5	Q9VW89	Q9VW89	PRELIMINARY: 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45
10	61.3	AA	117	10	Q9S778	Q9S778	PRELIMINARY: 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45
5	61.3	AA	119	5	Q45647	Q45647	PRELIMINARY: 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45
2	61.3	AA	226	2	Q9XW07	Q9XW07	PRELIMINARY: 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45


```

01 01-JAN-1948 (TREMblere1_06, Last sequence update)
02 01-MAY-2000 (TREMblere1_13, Last annotated update)
03 HYPOTHEITICAL PROTEIN M1672.
04 M1672.
05 Methanococcus jannaschii.
06 Archaeaea: Euryarchaeota; Methanococcales; Methanococcaceae;
07 Methanococcus.
08 NCBI_TaxID=2190;
09 11
10 SEQUENCE FROM N.A.
11 STRAIN=DSM 2661;
12 METLINE=95337999; PubMed 9489397;
13 Bolt G.J., White G., Olson G.J., Zhou L., Fleischmann R.D.,
14 Saitou N., Adams J.A., Eickholt J.D., Eickholt J.D.,
15 Kellaway A.E., Dougherty P.A., Smith R.G., Weiss R.R.,
16 Overbook J., Vekrellis P., Wilson R.F., Metcalf C.J.,
17 Scott J.L., Goodhagen N.S.M., Weisman C., Paulsen O.,
18 Ullrich T.E., Kelley J.M., Peterson J.L., Sadock P.W.,
19 Cotton M.D., Roberts K.M., Hunt R.A., Rhee H.P.,
20 Klink H.P., Fraser C.M., Smith R.G., Weiss R.R.,
21 *Complete genome sequence of the thermophilic archaeon,
22 jannaschii.*
23 Science 273:1058-1074(1995)
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
100
101
102
103
104
105
106
107
108
109
110
111
112
113
114
115
116
117
118
119
120
121
122
123
124
125
126
127
128
129
130
131
132
133
134
135
136
137
138
139
140
141
142
143
144
145
146
147
148
149
150
151
152
153
154
155
156
157
158
159
160
161
162
163
164
165
166
167
168
169
170
171
172
173
174
175
176
177
178
179
180
181
182
183
184
185
186
187
188
189
190
191
192
193
194
195
196
197
198
199
200
201
202
203
204
205
206
207
208
209
210
211
212
213
214
215
216
217
218
219
220
221
222
223
224
225
226
227
228
229
230
231
232
233
234
235
236
237
238
239
240
241
242
243
244
245
246
247
248
249
250
251
252
253
254
255
256
257
258
259
260
261
262
263
264
265
266
267
268
269
270
271
272
273
274
275
276
277
278
279
280
281
282
283
284
285
286
287
288
289
290
291
292
293
294
295
296
297
298
299
300
301
302
303
304
305
306
307
308
309
310
311
312
313
314
315
316
317
318
319
320
321
322
323
324
325
326
327
328
329
330
331
332
333
334
335
336
337
338
339
340
341
342
343
344
345
346
347
348
349
350
351
352
353
354
355
356
357
358
359
360
361
362
363
364
365
366
367
368
369
370
371
372
373
374
375
376
377
378
379
380
381
382
383
384
385
386
387
388
389
390
391
392
393
394
395
396
397
398
399
400
401
402
403
404
405
406
407
408
409
410
411
412
413
414
415
416
417
418
419
420
421
422
423
424
425
426
427
428
429
430
431
432
433
434
435
436
437
438
439
440
441
442
443
444
445
446
447
448
449
450
451
452
453
454
455
456
457
458
459
460
461
462
463
464
465
466
467
468
469
470
471
472
473
474
475
476
477
478
479
480
481
482
483
484
485
486
487
488
489
490
491
492
493
494
495
496
497
498
499
500
501
502
503
504
505
506
507
508
509
510
511
512
513
514
515
516
517
518
519
520
521
522
523
524
525
526
527
528
529
530
531
532
533
534
535
536
537
538
539
540
541
542
543
544
545
546
547
548
549
550
551
552
553
554
555
556
557
558
559
560
561
562
563
564
565
566
567
568
569
570
571
572
573
574
575
576
577
578
579
580
581
582
583
584
585
586
587
588
589
590
591
592
593
594
595
596
597
598
599
600
601
602
603
604
605
606
607
608
609
610
611
612
613
614
615
616
617
618
619
620
621
622
623
624
625
626
627
628
629
630
631
632
633
634
635
636
637
638
639
640
641
642
643
644
645
646
647
648
649
650
651
652
653
654
655
656
657
658
659
660
661
662
663
664
665
666
667
668
669
670
671
672
673
674
675
676
677
678
679
680
681
682
683
684
685
686
687
688
689
690
691
692
693
694
695
696
697
698
699
700
701
702
703
704
705
706
707
708
709
710
711
712
713
714
715
716
717
718
719
720
721
722
723
724
725
726
727
728
729
730
731
732
733
734
735
736
737
738
739
740
741
742
743
744
745
746
747
748
749
750
751
752
753
754
755
756
757
758
759
760
761
762
763
764
765
766
767
768
769
770
771
772
773
774
775
776
777
778
779
780
781
782
783
784
785
786
787
788
789
790
791
792
793
794
795
796
797
798
799
800
801
802
803
804
805
806
807
808
809
810
811
812
813
814
815
816
817
818
819
820
821
822
823
824
825
826
827
828
829
830
831
832
833
834
835
836
837
838
839
840
841
842
843
844
845
846
847
848
849
850
851
852
853
854
855
856
857
858
859
860
861
862
863
864
865
866
867
868
869
870
871
872
873
874
875
876
877
878
879
880
881
882
883
884
885
886
887
888
889
890
891
892
893
894
895
896
897
898
899
900
901
902
903
904
905
906
907
908
909
910
911
912
913
914
915
916
917
918
919
920
921
922
923
924
925
926
927
928
929
930
931
932
933
934
935
936
937
938
939
940
941
942
943
944
945
946
947
948
949
950
951
952
953
954
955
956
957
958
959
960
961
9
```

[illegible]

PT	"Conservation of structural domains and motifs (SOM) in the	
PT	structure and expression in vertebrates."	
RI	Mol Cell Biochem 148:119-126 (2000)	
DR	EMBL: AF220437; A0C28555.1;	
FT	NON TER	
FT	NON TER	1
SO	SEQUENCE	289 AA 3206 MB 077211.18-864081-087041

Query Match	79.2%	Score	44.15	Length	277
Best Local Similarity	87.5%	Pred. No.	92		
Matches	77	Conservative	1	Mismatches	67
QY	2	ERICPTCMV	9		
Db	223	ERICPTCMV	230		

RESULT	7
Q9HTM8	
ID	Q9HTM8
AC	Q9HTM8
PRELIMINARY;	
PRT;	16. AA

01-MAR-2001 (TREMBLEL_16) Created!
01-MAR-2001 (TREMBLEL_16) Last sequence update!
01-MAR-2001 (TREMBLEL_16) Last annotation update!
DE PROBABLE OXIDOREDUCTASE.
GN PA5327.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; gamma subdivision; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae
GC Pseudomonas.
GX NCBI_TaxId:287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN PAO1;
RA MEDLINE 20437497, PubMed-10984543
RA Stover J.C., Pham X.-Q.P., Fritsch A.L., Olson R.E.,
RA Hickey M.T., Robinson P.L., Hoff C.J., Davis K.A.,
RA Genter E.I., Collins I., Torgling E., Falkow-Warren S., Yu
RA Ardy L.L., Coulter S.N., Folmer K.R., Wad A., Larissa K., Lim
RA Smith K.A., Spencer D.H., Wong G.K.S., Holtz E.M.,
RA Polach J., Sauer M.D., Hancock K.W., Kelly S., Rice M.V.,
RT "Complete genome sequence of Pseudomonas aeruginosa PAO1,
RT opportunistic pathogen.";
RI Nature 406:684-694(2000).
DR EMBL: AF004945; AAC08712.1;
DR InterPro: IPRO01575;
DR Pfam: PF01565; FAD_Binding_4;
SO SEQUENCE 441 AA; 4945 MW; 02A6E56C174E7C9F4;

		77-190	Score 4 - 18-26	Total B 412
Very Match		77-190	Score 4 - 18-26	Total B 412
St Local Similarity		77-190	Pred. N = 1.4	
atches	6; Conservation	12; Misclassification	12; Trade-off	

RESULT	8
097860	
ID	097860
AC	097860
DT	01-MAY-1999 (TREMUR, 10, created)
DT	01-MAY-1999 (TREMUR, 10, last sequence update)
DT	01-MAY-2001 (TREMUR, 16, last seq. ref. update)
DE	TAYBATE-RESISTANT ACID PHOSPHATASE
OS	Oryctolagus cuniculus (Rabbit)
OC	Eukaryota; Metazoa; Chordata; Crinia; Vertebrata; Eumetazoa; Mammalia
GC	Mammalia; Eulharia; Lagomorpha; Leporidae; Oryctolagus
CX	NCBI_TaxID=99867
KN	[1]
RP	SEQUENCE FROM N.A.

NO	SERANJAMAN WHITE, LEECH, LEE, JONES
PX	MEDLINE 98A1476; PubMed-9751477
NA	KROEMER M., DE VRIES W.J.G.A.M., KUIJERS M.
RI	Kawashima H.
RJ	"Large scale isolation of oyster laccase by an improved method involving the preparation of a solidified cell NA library."
RL	Czechoslovakia 4409-475(1998).
CT	1. CATALYTIC ACTIVITY: AN OXYDATION OF 2-MNOL TO 2-HLZ BY AN ALCOHOL OXYDHIDROGENASE (BY SUPPLANTY).
ZK	LIFE, ABBOTT, G. EATON 979113
DK	Interpro: PROCONS41
DQ	InterPro: IPR014466
DG	Plant: PF02227; Pfam: phosphatase
RM	Hydrolase: Hydrolases
SD	SPONDINCE 3.45 AA; 46624 MW; 104827.7 cal/mol; 175 kcal/mol

Query Match	74.50%	Score = 6.2	Length = 4272
Best Local Similarity	80.00%	Percent = 7.7	
Matches	97	Missed = 0	Indels = 12
Cy	1	AAAGGTCATG	9
	1	1111111111	
Ddb	212	AAAGGTCATG	221

[illegible][illegible]

UNIT: MATHE
 Host: host.slm.com
 Mailbox: 52

09 2 FEBRUARY
 10 109 FEBRUARY 194

RESULT 10

000000

000000

000000

000000

000000

000000

000000

000000

000000

000000

000000

000000

000000

000000

000000

000000

000000

000000

000000

000000

000000

000000

000000

000000

000000

000000

000000

000000

000000

000000

000000

000000

000000

000000

000000

000000

000000

000000

000000

000000

000000

000000

000000

000000

000000

000000

000000

000000

000000

000000

000000

000000

000000

000000

000000

000000

000000

000000

000000

000000

000000

000000

000000

000000

000000

000000

000000

000000

000000

000000

000000

000000

000000

000000

000000

000000

000000

UNIT: MATHE
 Host: host.slm.com
 Mailbox: 52

09 2 FEBRUARY
 10 109 FEBRUARY 194

RESULT 10

000000

000000

000000

000000

000000

000000

000000

000000

000000

000000

000000

000000

000000

000000

000000

000000

000000

000000

000000

000000

000000

000000

000000

000000

000000

000000

000000

000000

000000

000000

000000

000000

000000

000000

000000

000000

000000

000000

000000

000000

000000

000000

000000

000000

000000

000000

000000

000000

000000

000000

000000

000000

000000

000000

000000

000000

000000

000000

000000

000000

000000

000000

000000

000000

000000

000000

000000

000000

000000

000000

000000

000000

000000

000000

000000

000000

000000

BC STRAIN-CDL:
 BA Catalano R.D., Vlad M., Kennedy R.C.,
 RI Submitted (DEC-1996) to the EMBL/GenBank/JDRI databases.
 DR EMBL: Y09878; CAA71005.1;
 SQ SEQUENCE 533 AA 6209 MW: 67551.6-24962.0997 11

Query Match 66.0%; Score 45.0; ID 11; Length 557;
 Best Local Similarity 100.0%; Pred. N. 76;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 4 HSPIC 7
 11111
 DB 234 HSPIC 238

RESULT 14
 G42902 PRELIMINARY PRI: 100% AA.

ID 042902 PRELIMINARY PRI: 100% AA.

AC 042902: P78753;

DT 01-JUN-1998 (TRENDEL 06, CROAT 3)

DT 01-JUN-1998 (TRENDEL 06, Last sequence update)

DT 01-MAR-2001 (TRENDEL 16, Last sequence update)

DT 01-MAR-2001 (TRENDEL 16, Last sequence update)

DT 01-MAR-2001 (TRENDEL 16, Last sequence update)

DT 01-MAR-2001 (TRENDEL 16, Last sequence update)

DT 01-MAR-2001 (TRENDEL 16, Last sequence update)

DT 01-MAR-2001 (TRENDEL 16, Last sequence update)

DT 01-MAR-2001 (TRENDEL 16, Last sequence update)

DT 01-MAR-2001 (TRENDEL 16, Last sequence update)

DT 01-MAR-2001 (TRENDEL 16, Last sequence update)

DT 01-MAR-2001 (TRENDEL 16, Last sequence update)

DT 01-MAR-2001 (TRENDEL 16, Last sequence update)

DT 01-MAR-2001 (TRENDEL 16, Last sequence update)

DT 01-MAR-2001 (TRENDEL 16, Last sequence update)

DT 01-MAR-2001 (TRENDEL 16, Last sequence update)

DT 01-MAR-2001 (TRENDEL 16, Last sequence update)

DT 01-MAR-2001 (TRENDEL 16, Last sequence update)

DT 01-MAR-2001 (TRENDEL 16, Last sequence update)

DT 01-MAR-2001 (TRENDEL 16, Last sequence update)

DT 01-MAR-2001 (TRENDEL 16, Last sequence update)

DT 01-MAR-2001 (TRENDEL 16, Last sequence update)

DT 01-MAR-2001 (TRENDEL 16, Last sequence update)

DT 01-MAR-2001 (TRENDEL 16, Last sequence update)

DT 01-MAR-2001 (TRENDEL 16, Last sequence update)

DT 01-MAR-2001 (TRENDEL 16, Last sequence update)

RESULT 15
 G98124 PRELIMINARY PRI: 100% AA.

ID G98124 PRELIMINARY PRI: 100% AA.

AC G98124 PRELIMINARY PRI: 100% AA.

DT 01-MAR-2001 (TRENDEL 16, CROAT 3)

DT 01-MAR-2001 (TRENDEL 16, Last sequence update)

DT 01-MAR-2001 (TRENDEL 16, Last sequence update)

DT 01-MAR-2001 (TRENDEL 16, Last sequence update)

DT 01-MAR-2001 (TRENDEL 16, Last sequence update)

DT 01-MAR-2001 (TRENDEL 16, Last sequence update)

DT 01-MAR-2001 (TRENDEL 16, Last sequence update)

DT 01-MAR-2001 (TRENDEL 16, Last sequence update)

DT 01-MAR-2001 (TRENDEL 16, Last sequence update)

DT 01-MAR-2001 (TRENDEL 16, Last sequence update)

DT 01-MAR-2001 (TRENDEL 16, Last sequence update)

DT 01-MAR-2001 (TRENDEL 16, Last sequence update)

DT 01-MAR-2001 (TRENDEL 16, Last sequence update)

DT 01-MAR-2001 (TRENDEL 16, Last sequence update)

DT 01-MAR-2001 (TRENDEL 16, Last sequence update)

DT 01-MAR-2001 (TRENDEL 16, Last sequence update)

DT 01-MAR-2001 (TRENDEL 16, Last sequence update)

DT 01-MAR-2001 (TRENDEL 16, Last sequence update)

DT 01-MAR-2001 (TRENDEL 16, Last sequence update)

DT 01-MAR-2001 (TRENDEL 16, Last sequence update)

DT 01-MAR-2001 (TRENDEL 16, Last sequence update)

DT 01-MAR-2001 (TRENDEL 16, Last sequence update)

DT 01-MAR-2001 (TRENDEL 16, Last sequence update)

DT 01-MAR-2001 (TRENDEL 16, Last sequence update)

DT 01-MAR-2001 (TRENDEL 16, Last sequence update)

DT 01-MAR-2001 (TRENDEL 16, Last sequence update)

DT 01-MAR-2001 (TRENDEL 16, Last sequence update)

DT 01-MAR-2001 (TRENDEL 16, Last sequence update)

DT 01-MAR-2001 (TRENDEL 16, Last sequence update)

DT 01-MAR-2001 (TRENDEL 16, Last sequence update)

DT 01-MAR-2001 (TRENDEL 16, Last sequence update)

DT 01-MAR-2001 (TRENDEL 16, Last sequence update)

Search completed: August 22, 2001, 14:11:12
 Job time: 202 sec

Query Match 66.0%; Score 45.0; ID 11; Length 557;

Best Local Similarity 100.0%; Pred. N. 76;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 4 HSPIC 7
 11111
 DB 234 HSPIC 238

PN US6194555.1.
 XX
 PD 27-FEB-2001.
 XX
 PE 07-JUN-1996: 96J8-0659254.
 XX
 PR 04-NOV-1995: 95J8-0538960.
 XX
 PA (UNITE-) UNIV TEXAS TECH HEALTH SCI CTR.
 XX
 PI Stocco DM, Clark RJ.
 XX
 DR WPI: 2001-0709472.
 DR N-PSDB: AAD02901, AAD02902.
 XX
 PT Novel nuclear acid encoding steroid hormone regulatory protein
 XX useful for treating steroid hormone-dependent disorders.
 PS
 XX Example 2: Fig 2: 41pp: English.
 CC The invention relates to steroid hormone regulatory proteins
 CC (STAR) and nuclear acid molecules encoding them. STAR proteins
 CC are used for regulating steroidogenesis. More particularly, these
 CC proteins are involved in regulating cholesterol transport into
 CC the mitochondria of a cell. The nuclear acid molecules of the
 CC invention are useful in gene therapy for the treatment of steroid
 CC hormone-dependent disorders, particularly, lipid congenital
 CC adrenal hyperplasia (CAH), infertility, sexual maturation,
 CC androgen-responsive tumors, precocious puberty, Klinefelter
 CC syndrome, adrenal hypoplasia congenita or hypoadrenal pitui-
 CC tary hypoadism. They are also useful for recombinant preparation
 CC of the steroidogenic acute regulatory protein.
 CC The present sequence is mouse steroidogenic acute regulatory
 CC protein (STAR).
 XX
 SO Sequence 284 AA:
 Query Match 100.0%: Start 1: 188-221: Length 244:
 Best Local Similarity: 100.0%: E-Val: 0.000000:
 Matches 11: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
 QY 1 11NNQPFQWKE 11
 1111111111
 Db 88 11nqpfqwkke 98
 RESULT 4
 AAW13238
 ID AAW13238 standard: Protein: 284 AA.
 AAW13238:
 DT 21-MAY 1997 (first entry)
 XX
 XX Human steroidogenesis acute regulatory protein mutant delta A4272.
 XX
 KW Human: steroidogenesis: acute regulatory protein: hSTAR: analysis:
 KW mutation: detection: prenatal: genetic: congenital: protein:
 KW lipid: adrenal: hyperplasia: treatment: prevention: gene:
 KW replacement: therapy: hypercholesterolemia: mutant.
 XX
 OS Homo sapiens.
 XX
 PN W09629338-A1.
 XX
 PD 26-SEP-1996.
 XX
 PE 22-MAR-1996: 96MO-0503896.
 XX
 PR 23-MAR-1995: 95US-0410540.
 XX
 PA (REGC-) UNIV CALIFORNIA.

IA (UNITE-) UNIV ILLINOISIANA
 XX
 PI Lit D, Miller WL, Strauss JF.
 XX
 DR WPI: 1996-44340/44.
 XX
 PT Isolated human steroidogenesis acute regulatory protein used
 XX for detection of mutation(s) of cholesterol biosynthetic
 XX lipid: adrenal: hyperplasia
 PS
 XX Claim 16: Page 1: 89pp: English.
 XX
 CC The present invention is the human steroidogenesis acute regulatory
 CC protein (STAR), recombinant lipid: adrenal: hyperplasia (CAH)
 CC associated mutant: delta A4272 (i.e. wild type: delta A4272 has
 CC been deleted). Analysis (the hSTAR gene for such a mutation is
 CC useful in the detection (e.g. prenatal) of CAH associated
 CC genetic defects or its transmission to children. CAH can be
 CC treated by protein or gene replacement therapy. Such can also be
 CC used to prevent or treat hypercholesterolemia.
 XX
 SO Sequence 284 AA:
 Query Match 91.9%: Start 1: 188-221: Length 244:
 Best Local Similarity: 90.9%: E-Val: 0.000000:
 Matches 10: Conservative 12: Mismatches 0: Indels 0: Gaps 0:
 QY 1 11NNQPFQWKE 11
 1111111111
 Db 89 11nqpfqwkke 99
 RESULT 5
 AAW13238
 ID AAW13238 standard: Protein: 284 AA.
 AAW13238:
 DT 21-MAY 1997 (first entry)
 XX
 XX Human steroidogenesis acute regulatory protein mutant Ala4272.
 XX
 KW Human: steroidogenesis: acute regulatory protein: hSTAR: analysis:
 KW mutation: detection: prenatal: genetic: congenital: protein:
 KW lipid: adrenal: hyperplasia: treatment: prevention: gene:
 KW replacement: therapy: hypercholesterolemia: mutant.
 XX
 OS Homo sapiens.
 XX
 PN W09629338-A1.
 XX
 PD 26-SEP-1996.
 XX
 PE 22-MAR-1996: 96MO-0503896.
 XX
 PR 23-MAR-1995: 95US-0410540.
 XX
 PA (REGC-) UNIV CALIFORNIA.
 XX
 PI Lit D, Miller WL, Strauss JF.
 XX
 DR WPI: 1996-44340/44.
 DR N-PSDB: AAD02901, AAD02902.
 XX
 PT Isolated human steroidogenesis acute regulatory protein gene used
 XX for detection of mutation(s) of cholesterol biosynthetic
 XX lipid: adrenal: hyperplasia

PT for detection of mutation(s) of this gene that cause congenital
 PT lipid adrenal hyperplasia
 XX
 PS Claim 1: Pages 62-64; 89pp; English.
 XX
 CC The present sequence is the human steroidogenesis acute
 CC regulatory protein (hSTAR). The hSTAR gene can be analysed for
 CC mutations to detect (e.g., prenatal) steroid defects associated
 CC with congenital lipid adrenal hyperplasia (CAH), or its
 CC transmission to children. CAH can be treated by protein or gene
 CC replacement therapy, which can also be used to prevent or treat
 CC hypercholesterolemia.
 CC A human adrenal cortex cDNA library was screened with a mouse STAR
 CC probe to isolate a 1.6 kb insert, inserting an ORF for a 285
 CC residue protein. When it was cloned into pSP65 and expressed in
 CC COS-1 cells cotransfected with pR458neo and pMX, it increased the
 CC level of progesterone synthesis from 15 percent of
 CC 20-alpha-hydroxycholesterol.
 CC
 XX
 SO Sequence 285 AA.

Query Match 91.9%; Score 576; DB 17; Length 285;
 Local Similarity 90.9%; Prod No. 1099;
 Matches 10; Conservative 1; Mismatches 0; Indels 1; Gaps 0
 QY 1 LNNQEWKKE 11
 II:IIIIIIII
 DB 89 LNNQEWKKE 99

RESULT 8
 AAW13233
 ID AAW13233 standard; protein; 285 AA.
 XX
 AC AAW13233;
 XX
 DI 21-MAY-1997 (first entry)
 XX
 DE Human steroidogenesis acute regulatory protein mutant (glucocorticoid).
 XX
 KW Human steroidogenesis acute regulatory protein; hSTAR; analysis;
 KW mutation; detection; prenatal; defect; congenital; protein;
 KW lipid adrenal hyperplasia; treatment; prevention; gene;
 KW replacement therapy; hypercholesterolemia; mutant.
 XX
 OS Homo sapiens.
 XX
 FH Key location/Qualifiers
 FT Misc-difference 169 /note "Wild type Glu substituted with Cys"
 XX
 W09629348-A1
 XX
 PU 26-SEP-1996.
 XX
 PF 22-MAR-1996; 96MO-0503896.
 XX
 PR 23-MAR-1995; 95US-0410540.
 XX
 PA (REGG) UNIV CALIFORNIA.
 PA (TYPE-) UNIV PENNSYLVANIA.
 XX
 PI Lin D, Miller ML, Strauss JF;
 DR WPI: 1996-44343/44.
 DR N-PSDB: AAT62013.
 XX
 PT Isolated human steroidogenesis acute regulatory protein gene used
 PT for detection of mutation(s) of this gene that cause congenital
 PT lipid adrenal hyperplasia
 XX
 PS Claim 13; Page 7; 89pp; English.

XX
 CC The present sequence is the human steroidogenesis acute regulatory
 CC protein (hSTAR), congenital lipid adrenal hyperplasia (CAH)
 CC associated mutant. Analysing the hSTAR gene for such a
 CC mutation is useful in the detection (e.g., prenatal) of CAH
 CC associated genetic defects, or its transmission to children. CAH
 CC can be treated by protein or gene replacement therapy, which can
 CC also be used to prevent or treat hypercholesterolemia.
 XX
 SO Sequence 285 AA;
 Query Match 91.9%; Score 576; DB 17; Length 285;
 Local Similarity 90.9%; Prod No. 1099;
 Matches 10; Conservative 1; Mismatches 0; Indels 1; Gaps 0
 QY 1 LNNQEWKKE 11
 II:IIIIIIII
 DB 89 LNNQEWKKE 99

RESULT 9
 AAW13234
 ID AAW13234 standard; protein; 285 AA
 XX
 AC AAW13234;
 XX
 DI 21-MAY-1997 (first entry)
 XX
 DE Human steroidogenesis acute regulatory protein mutant (Androgen).
 XX
 KW Human steroidogenesis acute regulatory protein; hSTAR; analysis;
 KW mutation; detection; prenatal; defect; congenital; protein;
 KW lipid adrenal hyperplasia; treatment; prevention; gene;
 KW replacement therapy; hypercholesterolemia; mutant.
 XX
 OS Homo sapiens.
 XX
 FH Key location/Qualifiers
 FT Misc-difference 162 /note "Wild type Pro substituted with Leu"
 XX
 W09629348-A1
 XX
 PU 26-SEP-1996.
 XX
 PF 22-MAR-1996; 96MO-0503896.
 XX
 PR 23-MAR-1995; 95US-0410540.
 XX
 PA (REGG) UNIV CALIFORNIA.
 PA (TYPE-) UNIV PENNSYLVANIA.
 XX
 PI Lin D, Miller ML, Strauss JF;
 DR WPI: 1996-44343/44.
 DR N-PSDB: AAT62013.
 XX
 PT Isolated human steroidogenesis acute regulatory protein gene used
 PT for detection of mutation(s) of this gene that cause congenital
 PT lipid adrenal hyperplasia
 XX
 PS Claim 13; Page 7; 89pp; English.
 CC The present sequence is the human steroidogenesis acute regulatory
 CC protein (hSTAR), congenital lipid adrenal hyperplasia (CAH)
 CC associated mutant. Analysing the hSTAR gene for such a
 CC mutation is useful in the detection (e.g., prenatal) of CAH
 CC associated genetic defects, or its transmission to children. CAH
 CC can be treated by protein or gene replacement therapy, which can
 CC also be used to prevent or treat hypercholesterolemia.
 XX
 SO Sequence 285 AA;

Report Month: 08/01/97
Host: Local: Stimulants: 00/00/00
Methods: 00/00/00
07 1 11NNDJMKK: 11
08 09 11NDJMKK: 09

Report Month: 08/01/97
Host: Local: Stimulants: 00/00/00
Methods: 00/00/00
07 1 11NNDJMKK: 11
08 09 11NDJMKK: 09

Report Month: 08/01/97
Host: Local: Stimulants: 00/00/00
Methods: 00/00/00
07 1 11NNDJMKK: 11
08 09 11NDJMKK: 09

Report Month: 08/01/97
Host: Local: Stimulants: 00/00/00
Methods: 00/00/00
07 1 11NNDJMKK: 11
08 09 11NDJMKK: 09

Report Month: 08/01/97
Host: Local: Stimulants: 00/00/00
Methods: 00/00/00
07 1 11NNDJMKK: 11
08 09 11NDJMKK: 09

Report Month: 08/01/97
Host: Local: Stimulants: 00/00/00
Methods: 00/00/00
07 1 11NNDJMKK: 11
08 09 11NDJMKK: 09

Report Month: 08/01/97
Host: Local: Stimulants: 00/00/00
Methods: 00/00/00
07 1 11NNDJMKK: 11
08 09 11NDJMKK: 09

Report Month: 08/01/97
Host: Local: Stimulants: 00/00/00
Methods: 00/00/00
07 1 11NNDJMKK: 11
08 09 11NDJMKK: 09

Report Month: 08/01/97
Host: Local: Stimulants: 00/00/00
Methods: 00/00/00
07 1 11NNDJMKK: 11
08 09 11NDJMKK: 09

Report Month: 08/01/97
Host: Local: Stimulants: 00/00/00
Methods: 00/00/00
07 1 11NNDJMKK: 11
08 09 11NDJMKK: 09

Report Month: 08/01/97
Host: Local: Stimulants: 00/00/00
Methods: 00/00/00
07 1 11NNDJMKK: 11
08 09 11NDJMKK: 09

Report Month: 08/01/97
Host: Local: Stimulants: 00/00/00
Methods: 00/00/00
07 1 11NNDJMKK: 11
08 09 11NDJMKK: 09

Report Month: 08/01/97
Host: Local: Stimulants: 00/00/00
Methods: 00/00/00
07 1 11NNDJMKK: 11
08 09 11NDJMKK: 09

Report Month: 08/01/97
Host: Local: Stimulants: 00/00/00
Methods: 00/00/00
07 1 11NNDJMKK: 11
08 09 11NDJMKK: 09

Report Month: 08/01/97
Host: Local: Stimulants: 00/00/00
Methods: 00/00/00
07 1 11NNDJMKK: 11
08 09 11NDJMKK: 09

Report Month: 08/01/97
Host: Local: Stimulants: 00/00/00
Methods: 00/00/00
07 1 11NNDJMKK: 11
08 09 11NDJMKK: 09

Sequence 285 AA:

Query Match 91.98% Score 5.11 E-22 Length 285
Best Local Similarity 90.98% Pred. No. 1397
Matches 10: Conservative 1: Mismatch 0: Indels 0: Gaps

DB 89 L11NQGKWK 99

RESULT 12

AAW74155

ID AAW74155 standard: protein: 12 AA

AAW74155:

05-MAY-1999 (first entry)

Mouse steroidogenic acute regulatory protein tryptic peptide

STAR: steroidogenic acute regulatory protein: Mouse Albright's syndrome steroid hormone dependent disorder; adrenal hyperplasia congenital (CAH); lipid congenital adrenal hyperplasia; infertility; sexual maturation androgen-responsive tumours; hypoadrenalism; therapy: progesterone level

Mus sp.

US5872246-A.

16-FEB-1999.

04-NOV-1995: 9508-0538960.

04-NOV-1995: 9508-0538960.

(BYTE) UNIV TEXAS TECH HEALTH SCI CENT

Clark RJ. Stereo DM;

WP1: 1999-166720/14

New nucleic acid encoding steroidogenic acute regulatory protein useful for treatment of steroid hormone dependent disorders such as lipid congenital adrenal hyperplasia, infertility and androgen-responsive tumours

Example 2: Column 26: 25pp; English.

This sequence is a tryptic peptide fragment of the steroidogenic acute regulatory protein (STAR) of the mouse. The STAR protein is an enzyme that catalyzes the conversion of cholesterol to androgens and its products or derivatives may be used as precursors and primers for the synthesis of androgens. The STAR protein is also involved in the regulation of steroid hormone dependent disorders such as lipid congenital adrenal hyperplasia (CAH), infertility, sexual maturation, androgen-responsive tumours, precocious puberty, McCune Albright syndrome, adrenal hyperplasia congenital and hypoadrenalism. Monitoring levels of STAR may also indicate reduced progesterone levels and so a risk of spontaneous abortion.

Sequence 12 AA:

Query Match 83.98% Score 5.11 E-22 Length 12
Best Local Similarity 100.00% Pred. No. 0: 0: Indels 0: Gaps
Matches 9: Conservative 0: Mismatch 0: Indels 0: Gaps

DB 1 L11NQGKWK 9

4 L11NQGKWK 12

RESULT 13

AAV72833

ID AAV72833 standard: peptide: 12 AA

AAV72833:

31-MAY-2001 (first entry)

Mouse tryptic peptide #25 for analysis of STAR protein.

Mouse steroidogenic acute regulatory protein: STAR gene; hereditary steroid hormone dependent disorders; CAH; lipid congenital adrenal hyperplasia; infertility; sexual maturation androgen-responsive tumours; hypoadrenalism; therapy: progesterone level; adrenal hyperplasia congenital; cytochrome P450c17

Mus sp.

US6194555-B1.

27-FEB-2001.

07-JUN-1996: 9508-0538960.

04-NOV-1995: 9508-0538960.

(BYTE) UNIV TEXAS TECH HEALTH SCI CENT

Stereo DM; Clark RJ;

WP1: 2001-217346/22.

New nucleic acid encoding steroid hormone dependent regulatory protein useful for treatment of steroid hormone dependent disorders

Example 2: Column 28: 41pp; English

The invention relates to steroid dependent regulatory protein (STAR) and nucleic acid molecules encoding them. STAR proteins are used for regulating steroidogenesis. More particularly, these proteins are involved in regulating the metabolism of cholesterol in the mitochondria of a cell. The nucleic acid molecules of the invention are useful in gene therapy for the treatment of steroid hormone-dependent disorders, particularly lipid congenital adrenal hyperplasia (CAH), infertility, sexual maturation, androgen-responsive tumours, precocious puberty, McCune Albright syndrome, adrenal hyperplasia congenital, hypoadrenalism, and hypogonadism. They are also useful for recombinant preparation of the steroidogenic acute regulatory protein. The present sequence is tryptic peptide #25. The peptide is used in the cloning and sequence analysis of cDNA encoding the 20kDa form of STAR protein. This peptide is also used in the analysis of the STAR protein sequence and as a primer for the PCR for detection of polymorphisms for screening and identifying antigenic determinants of STAR protein.

Sequence 12 AA:

Query Match 83.98% Score 5.11 E-22 Length 12
Best Local Similarity 100.00% Pred. No. 0: 0: Indels 0: Gaps
Matches 9: Conservative 0: Mismatch 0: Indels 0: Gaps

DB 1 L11NQGKWK 9

4 L11NQGKWK 12

RESULT 14

AAW60936

ID AAW60936 standard: protein: 200 AA

AAW60936:

[illegible][illegible][illegible]



NUMBER OF SEQUENCES: 19
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: AKIN, GARY, STRAUSS, HARRY & FELD, L.L.P.
 STREET: 1900 Frost Bank Plaza, R.F. Vantage Avenue
 CITY: Austin
 STATE: TX
 COUNTRY: U.S.A.
 ZIP: 78701
 COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-IMS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: 08/08/659 54
 FILING DATE: 07-JUN-1996
 CLASSIFICATION: 540
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/538,760
 FILING DATE: 04-06-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Mayfield, Denise E.
 PRELIMINARY NUMBER: 43,742
 REFERENCE/DOCKET NUMBER: 43375 0000
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 512/499-6200
 TELEFAX: 512/499-6299
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 6 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-659-254-6

Query Match 61.3% Score 189 PB 42 Length 63
 Best Local Similarity 100.0% Pctd. No. 1 100.0%
 Matches 6: Conservative 0: Miscellaneous 0: Gaps 0:

QY 4 NORQWK 9
 111111
 DB 1 NORQWK 6

RESULT 11
 US-08-815-176-1
 Sequence 1, Application US/08815176
 Patent No. 5874224
 GENERAL INFORMATION:
 APPLICANT: Bandman, Tony
 APPLICANT: Diebold, Tony
 TITLE OF INVENTION: NOVEL BOP KINETIC BINDING PROTEIN
 NUMBER OF SEQUENCES: 1
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Icyto Pharmaceuticals, Inc.
 STREET: 3174 Porter Dr.
 CITY: Palo Alto
 STATE: CA
 COUNTRY: USA
 ZIP: 94304
 COMPUTER READABLE FORM:
 MEDIUM TYPE: diskette
 COMPUTER: IBM compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FASTSEQ for Windows Ver 1.0.2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: 08/08/815 176
 FILING DATE: Filed Herewith
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:

ATTORNEY/AGENT INFORMATION:
 NAME: Billings, Lucy J.
 REGISTRATION NUMBER: 46,749
 REFERENCE/DOCKET NUMBER: 44-023 03
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-865-0555
 TELEFAX: 415-845-4166
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 450 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 MAPPING SCHEME:
 LIBRARY: GENBANK
 CLONE: 1291904
 US-08-815-176-1

Query Match 58.1% Score 178 PB 42 Length 430
 Best Local Similarity 70.0% Pctd. No. 2 100.0%
 Matches 72: Conservative 12: Miscellaneous 2: Gaps 0:

QY 1 INNORQWK 10
 11111111
 DB 27 INNORQWK 06

RESULT 12
 US-08-485-947-12
 Sequence 12, Application US/08485047
 Patent No. 5962634
 GENERAL INFORMATION:
 APPLICANT: Muller, Daniel
 APPLICANT: Asanelli, Elise
 APPLICANT: Zellerbach, Katherine
 APPLICANT: Wallace, Linda
 TITLE OF INVENTION: Cysteine protease inhibitor
 TITLE OF INVENTION: Cysteine protease inhibitor
 NUMBER OF SEQUENCES: 13
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Banner & Allergent, LLC
 STREET: 10 S. Wacker Drive Suite 1000
 CITY: Chicago
 STATE: IL
 COUNTRY: USA
 ZIP: 60606
 COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: 08/08/485 947
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/474,473
 FILING DATE: 18-MAY-1995
 APPLICATION NUMBER: WO 97/289 70002
 FILING DATE: 15-JUL-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/913 043
 FILING DATE: 17-JUL-1992
 ATTORNEY/AGENT INFORMATION:
 NAME: McLaughlin, John J.
 REGISTRATION NUMBER: 25,949
 REFERENCE/DOCKET NUMBER: 9401
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (312) 215-1000
 TELEFAX: (312) 715-1244
 INFORMATION FOR SEQ ID NO: 12:

GENERAL INFORMATION:

APPLICANT: Chinnadurai, Govindasamy
 TITLE OF INVENTION: APOPTOSIS REGULATING PROTEINS
 NUMBER OF SEQUENCES: 35
 CORRESPONDENCE ADDRESS:
 ADDRESS: SUGHRUE, MIRON, ZIMM, MACKEY & SEAS
 STREET: 2100 Pennsylvania Avenue, N.W.
 CITY: Washington
 STATE: D.C.
 COUNTRY: USA
 ZIP: 20047
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0 V1.00 #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/408,045
 FILING DATE: 21-MAR-1995
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Mack, Susan J.
 REGISTRATION NUMBER: 40,951
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 293-7060
 TELEFAX: (202) 293-7060
 INFORMATION FOR SEQ. ID NO: 21:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 228 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-408-095-21

Query Match

54.88; Score 34; 08.2; Length 228;

Best local Similarity 50.08; Pred. No. 1;

Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 ILNNQETWKK 10

DB 88 MLSNDASWKK 97

Search completed: August 22, 2001, 14:33:11
 Job time: 367 sec



Genome version: 1.0
Copyright (c) 1993 - 2000 Empress Ltd.

OM protein - protein search, using SW mode

Run on: August 22, 2001, 14:25:29 Search time 61.3 seconds
(without alignment)

12,994 Million cell updates/second

Title: us-08-659-254-8

Perfect score: 62

Sequence: 1 LENROCKMKE 11

Scoring table: BLOSUM62

Gap: 10.0, Gapext: 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Post-processing: Minimum Match: 0%

Maximum Match: 100%

Database: 1: PIR-68**

2: PIR-2**

3: PIR-3**

4: PIR-4**

Prod. No. is the number of results returned by query to have a

score greater than or equal to the score of the result being displayed.

and is derived by analysis of the results returned by the query.

SIKMA0111

Result No.	Score	Query Match Length	DB ID	Accession	Description
1	62	100.0	284	2 A55455	steroidogenic acute regulatory protein (house mouse)
2	62	100.0	362	2 J05385	steroidogenic acute regulatory protein (house mouse)
3	57	91.9	285	2 J38248	steroidogenic acute regulatory protein (house mouse)
4	51	82.3	285	2 J04115	steroidogenic acute regulatory protein (house mouse)
5	43	69.4	157	2 S62571	steroidogenic acute regulatory protein (house mouse)
6	42	67.7	783	2 J05477	steroidogenic acute regulatory protein (house mouse)
7	42	67.7	924	2 J05477	steroidogenic acute regulatory protein (house mouse)
8	41	66.1	800	2 F64568	steroidogenic acute regulatory protein (house mouse)
9	40	64.5	620	2 F64568	steroidogenic acute regulatory protein (house mouse)
10	40	64.5	1511	2 A53151	steroidogenic acute regulatory protein (house mouse)
11	40	64.5	1524	2 S84694	steroidogenic acute regulatory protein (house mouse)
12	39	62.9	179	2 S36255	steroidogenic acute regulatory protein (house mouse)
13	39	62.9	847	1 A53800	steroidogenic acute regulatory protein (house mouse)
14	39	62.9	1711	2 J31337	steroidogenic acute regulatory protein (house mouse)
15	39	62.9	1742	2 J31337	steroidogenic acute regulatory protein (house mouse)
16	38	61.3	119	2 J03238	steroidogenic acute regulatory protein (house mouse)
17	38	61.3	480	2 E86659	steroidogenic acute regulatory protein (house mouse)
18	38	61.3	1588	1 HWY041	steroidogenic acute regulatory protein (house mouse)
19	37	59.7	446	2 J11058	steroidogenic acute regulatory protein (house mouse)
20	37	59.7	458	2 S31467	steroidogenic acute regulatory protein (house mouse)
21	37	59.7	490	2 J34192	steroidogenic acute regulatory protein (house mouse)
22	37	59.7	590	2 S62571	steroidogenic acute regulatory protein (house mouse)
23	37	59.7	800	2 A29034	steroidogenic acute regulatory protein (house mouse)
24	37	59.7	822	2 J10632	steroidogenic acute regulatory protein (house mouse)
25	37	59.7	947	2 J49645	steroidogenic acute regulatory protein (house mouse)
26	37	59.7	1245	2 J31337	steroidogenic acute regulatory protein (house mouse)
27	37	59.7	1271	2 J64247	steroidogenic acute regulatory protein (house mouse)
28	37	59.7	1289	2 J72334	steroidogenic acute regulatory protein (house mouse)
29	36	58.1	112	2 J06921	steroidogenic acute regulatory protein (house mouse)

30	36	58.1	171	2 E82743	steroidogenic acute regulatory protein (house mouse)
31	36	58.1	189	2 S34309	steroidogenic acute regulatory protein (house mouse)
32	36	58.1	194	2 J01824	steroidogenic acute regulatory protein (house mouse)
33	36	58.1	430	2 J00376	steroidogenic acute regulatory protein (house mouse)
34	36	58.1	453	2 S86262	steroidogenic acute regulatory protein (house mouse)
35	36	58.1	466	2 S4810	steroidogenic acute regulatory protein (house mouse)
36	36	58.1	468	2 J50274	steroidogenic acute regulatory protein (house mouse)
37	36	58.1	493	2 J48444	steroidogenic acute regulatory protein (house mouse)
38	36	58.1	403	2 J44844	steroidogenic acute regulatory protein (house mouse)
39	36	58.1	458	2 J71557	steroidogenic acute regulatory protein (house mouse)
40	36	58.1	467	2 J68435	steroidogenic acute regulatory protein (house mouse)
41	36	58.1	505	2 S68244	steroidogenic acute regulatory protein (house mouse)
42	36	58.1	527	2 J45212	steroidogenic acute regulatory protein (house mouse)
43	36	58.1	780	2 J25710	steroidogenic acute regulatory protein (house mouse)
44	36	58.1	799	1 J06861	steroidogenic acute regulatory protein (house mouse)
45	36	58.1	877	2 J64890	steroidogenic acute regulatory protein (house mouse)

ALL 200111

RESULT

A55455

steroidogenic acute regulatory protein (house mouse)

C.Species: Mus musculus (house mouse)

C.Sequence: 10 Feb 1997, sequence_level: 1, 100.0% identity, 100.0% coverage

C.Accession: A55455

C.Protein: 100.0% identity, 100.0% coverage

C.Protein: 100.0% identity, 100.0% coverage

C.Protein: 100.0% identity, 100.0% coverage

C.Protein: 100.0% identity, 100.0% coverage

C.Protein: 100.0% identity, 100.0% coverage

C.Protein: 100.0% identity, 100.0% coverage

C.Protein: 100.0% identity, 100.0% coverage

C.Protein: 100.0% identity, 100.0% coverage

C.Protein: 100.0% identity, 100.0% coverage

C.Protein: 100.0% identity, 100.0% coverage

C.Protein: 100.0% identity, 100.0% coverage

C.Protein: 100.0% identity, 100.0% coverage

C.Protein: 100.0% identity, 100.0% coverage

C.Protein: 100.0% identity, 100.0% coverage

C.Protein: 100.0% identity, 100.0% coverage

C.Protein: 100.0% identity, 100.0% coverage

C.Protein: 100.0% identity, 100.0% coverage

C.Protein: 100.0% identity, 100.0% coverage

C.Protein: 100.0% identity, 100.0% coverage

C.Protein: 100.0% identity, 100.0% coverage

C.Protein: 100.0% identity, 100.0% coverage

C.Protein: 100.0% identity, 100.0% coverage

C.Protein: 100.0% identity, 100.0% coverage

C.Protein: 100.0% identity, 100.0% coverage

Query Match 67.7% Score 42.78 Length 78
 Best local similarity 77.8% Prot. No. 21
 Matches 7: Conservative 11 Mismatches 0 Indels 0 Gaps 0

QY 1 LNNOECKM 9
 DB 201 LNNOECKM 200

RESULT 7

Cellulase (EC 3.2.1.4), alkaline, Bacillus sp. (strain KSM-5237)
 N.Altitude names: endo-1,4-beta-glucanase
 C.Species: Bacillus sp. (strain KSM-5237)
 C.Date: 31 Mar 2001 #sequence revision: 11 04 2001 #date of last update
 C.Accession: J07532; p7107
 R.Hayamada, Y.; Hataida, Y.; Koike, K.; Yoshida, T.; Kashi, S.; Kikuchi, T.; Iino, H.
 Biosci. Biotechnol. Biobiom. 44, 2281-2289, 2000
 A.Title: Deduced amino acid sequence and possible catalytic residues of a thermostable
 A.Reference number: J07532; M01D:2104686
 A.Accession: J07532

A.Molecule type: DNA
 A.Studies: 1-824 <HAR>
 A.Cross-references: J084:AB019420
 A.Experimental source: strain KSM-5247
 A.Accession: J07107
 A.Molecule type: protein
 A.Residues: 31-50 <HA2>
 C.Comment: This enzyme is a thermostable cellulase enzyme used as effective reagent as
 C.Gonolysis:
 A.Gene: Eql-237
 C.Keywords: hydrolase, glycosidase

Query Match 67.7% Score 42.78 Length 824
 Best local similarity 77.8% Prot. No. 21
 Matches 7: Conservative 11 Mismatches 0 Indels 0 Gaps 0

QY 1 LNNOECKM 9
 DB 201 LNNOECKM 200

RESULT 8

Protein H1672: Methanococcus Janaschii
 C.Species: Methanococcus Janaschii
 C.Date: 15 Sep 1994 #sequence revision: 15 Sep 1994 #length: 230
 C.Accession: F64508
 R.H. J. D. Sadow, P.W. Hanna, M.C. Jellison, M.D. Roberts, K.M. Hunt, M.A.
 Science 273, 1058-1074, 1996
 A.Authors: Kaine, R.P.; Berchowsky, M.; Voth, H.P.; Fraser, C.H.; Smith, W.C.;
 A.Title: Complete genome sequence of the methanogenic archaeon Methanococcus Janaschii
 A.Reference number: A54300; M01D:9634799
 A.Accession: F64508
 A.Molecule type: DNA
 A.Status: preliminary; nucleic acid sequence not shown; sequencing not done
 A.Residues: 1-800 <H1672>
 A.Cross-references: G8:067607; G8:177117; G8:177117; F:08:AB000001; F:08:AB000002; F:
 C.Gonolysis:
 A.Map position: REV1656207-1654805

Query Match 66.1% Score 4.48 Length 200
 Best local similarity 64.5% Prot. No. 47
 Matches 6: Conservative 11 Mismatches 4 Indels 0 Gaps 0

QY 1 LNNOECKM 11
 DB 255 LNNOECKM 265

Query Match 64.5% Score 4.48 Length 200
 Best local similarity 60.0% Prot. No. 47
 Matches 6: Conservative 11 Mismatches 4 Indels 0 Gaps 0

QY 2 LNNOECKM 1
 DB 13 LNNOECKM 22

RESULT 9

Hypothetical protein Y08014w: yeast (Saccharomyces cerevisiae)
 N.Altitude names: hypothetical protein Y08014
 C.Species: Saccharomyces cerevisiae
 C.Date: 17 May 1994 #sequence revision: 17 May 1994 #date of last update
 C.Accession: S64304
 R.Kobayashi, M.; Mueller, A.; S. Brueckner, M.; Thoden, M.
 submitted to the Protein Sequence Database, March 1994
 A.Reference number: S64304
 A.Accession: S64304
 A.Molecule type: DNA
 A.Residues: 1-620 <HAR>
 A.Cross-references: J08:072746; M01:010000; F:08:AB000001; F:08:AB000002
 A.Experimental source: strain S288c
 C.Gonolysis:
 A.Gene: Y08014w
 A.Map position: 78

Query Match 64.5% Score 4.48 Length 200
 Best local similarity 60.0% Prot. No. 47
 Matches 6: Conservative 11 Mismatches 4 Indels 0 Gaps 0

QY 2 LNNOECKM 1
 DB 13 LNNOECKM 22

Query Match 64.5% Score 4.48 Length 200
 Best local similarity 60.0% Prot. No. 47
 Matches 6: Conservative 11 Mismatches 4 Indels 0 Gaps 0

QY 2 LNNOECKM 1
 DB 13 LNNOECKM 22

Query Match 64.5% Score 4.48 Length 200
 Best local similarity 60.0% Prot. No. 47
 Matches 6: Conservative 11 Mismatches 4 Indels 0 Gaps 0

QY 2 LNNOECKM 1
 DB 13 LNNOECKM 22

Query Match 64.5% Score 4.48 Length 200
 Best local similarity 60.0% Prot. No. 47
 Matches 6: Conservative 11 Mismatches 4 Indels 0 Gaps 0

QY 2 LNNOECKM 1
 DB 13 LNNOECKM 22

Query Match 64.5% Score 4.48 Length 200
 Best local similarity 60.0% Prot. No. 47
 Matches 6: Conservative 11 Mismatches 4 Indels 0 Gaps 0

QY 2 LNNOECKM 1
 DB 13 LNNOECKM 22

QY 2 LNNOECKM 1
 DB 13 LNNOECKM 22

||||| 31
ID 396 Q85WKE 402

RESULT 14

T1337

1,4-Beta-glucanase (EC 3.2.1.-) - *Anaerococcus thermophilum* (Triton)C:Species: *Anaerococcus thermophilum*

C:Date: 02-Sep-2000 #sequence_revision 2307200 #text_change 02-Sep-2000

C:Accession: T1337

R:Zverlov, V.; Mahu, S.; Kiedel, K.; Hennrich, K.

Microbiology 144, 457-465, 1998

A:Title: Properties and gene structure of a filamentous cellulolytic enzyme (CelA) from *Anaerococcus thermophilus*

A:Reference number: Z1003; MUID:9815444

A:Accession: T1337

A:Status: preliminary; translated from JG/MB/2000

A:Molecule type: DNA

A:Residues: 1-1711 <ZVE>

A:Cross-references: EMBL:Z86105; MIM:6117120; EMBL:6054; EMBL:AB03700

C:Genetics:

A:Gene: celA

C:Keywords: glycosidase; hydrolase

Query Match

62.9% Score 99 LB 23 Length 1711

Best Local Similarity 75.6% Pred. No. 180-123

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0

QY 1 LNNOCW 8

ID 478 LVNOSGW 485

RESULT 15

T17120

cellulase (EC 3.2.1.-) precursor, thermophilic *Caldocellum saccharolyticum*C:Species: *Caldocellum saccharolyticum*

C:Date: 15-Oct-1999 #sequence_revision 15000 #text_change 17-Nov-2000

C:Accession: T17120; A43745

R:Terro, V.S.; Saul, D.J.; Bergquist, P.L.

Appl. Microbiol. Biotechnol. 45, 291-296, 1997

A:Title: CelA, another gene coding for a multidomain cellulase from the extreme thermophilic

A:Reference number: Z18698; MUID:95346704

A:Accession: T17120

A:Status: preliminary; translated from GY/MB/2000

A:Molecule type: DNA

A:Residues: 1-1742 <TEO>

A:Cross-references: EMBL:L32712; NID:457400; EMBL:AA91000; EMBL:AA91001

R:Bluerich, E.; Rhana Vaswani, N.; Grayling, A.; Lowe, D.R.; Bergquist, P.L.

Environ. Microbiol. 57, 694-700, 1997

A:Title: Cloning, sequence analysis, and expression in *Escherichia coli* of a gene coding

A:Reference number: A43745; MUID:91247815

A:Accession: A43745

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1516-1544, 'A', 1546-1742 <LNE>

A:Cross-references: EMBL:M36053; NID:441202; EMBL:AA428601; EMBL:AA428602

C:Genetics:

A:Gene: celA

C:Keywords: glycosidase; hydrolase

Query Match

62.9% Score 99 LB 23 Length 1742

Best Local Similarity 75.0% Pred. No. 180-123

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0

QY 1 LNNOCW 8

ID 501 LVNOSGW 508

Search completed: August 22, 2001, 14:27:33
Job time: 84 sec

Wed Aug 22 15:43:04 2001

us-08-659-254-8.rpt

Page 6

Wed Aug 22 15:43:03 2001

us-08-659-254-7.rpr

Page 6

GeneCard Worksheet
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw mode

Run on: August 22, 2001, 14:30:53 : server: 130.25.8.200

(without alignment)

8,012 Million test of 145,000

Title: us-08-659-254-7

51

Perfect score:

1 ACH:PTCOW 9

Scoring table:

Gap:10.0, Gapext:0.5

Searched:

94435 seqs, 44255486 pos, 2000

Total number of hits satisfying chosen parameters: 94435

Minimum DB seq length: 0

Minimum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summations

Database: Swissprot_39.*

Pred. No. is the number of results produced by chance to have a score greater than or equal to the score of the result having predicted and is derived by analysis of the total score distribution.

Result No.	Score	Query Match length DB	ID	SWMAP	Description
1	53	100.0	284	1	STAR-MOL: 177827, 141000000
2	53	100.0	284	1	STAR-MOL: 177827, 141000000
3	53	100.0	285	1	STAR-MOL: 177827, 141000000
4	53	100.0	285	1	STAR-MOL: 177827, 141000000
5	53	100.0	285	1	STAR-MOL: 177827, 141000000
6	53	100.0	285	1	STAR-MOL: 177827, 141000000
7	45	84.9	284	1	STAR-MOL: 177827, 141000000
8	39.5	74.5	327	1	PPAS-MOL: 177827, 141000000
9	39.5	74.5	327	1	PPAS-MOL: 177827, 141000000
10	39.5	74.5	327	1	PPAS-MOL: 177827, 141000000
11	39.5	74.5	327	1	PPAS-MOL: 177827, 141000000
12	39.5	74.5	327	1	PPAS-MOL: 177827, 141000000
13	39.5	74.5	327	1	PPAS-MOL: 177827, 141000000
14	39.5	74.5	327	1	PPAS-MOL: 177827, 141000000
15	39.5	74.5	327	1	PPAS-MOL: 177827, 141000000
16	39.5	74.5	327	1	PPAS-MOL: 177827, 141000000
17	39.5	74.5	327	1	PPAS-MOL: 177827, 141000000
18	39.5	74.5	327	1	PPAS-MOL: 177827, 141000000
19	39.5	74.5	327	1	PPAS-MOL: 177827, 141000000
20	39.5	74.5	327	1	PPAS-MOL: 177827, 141000000
21	39.5	74.5	327	1	PPAS-MOL: 177827, 141000000
22	39.5	74.5	327	1	PPAS-MOL: 177827, 141000000
23	39.5	74.5	327	1	PPAS-MOL: 177827, 141000000
24	39.5	74.5	327	1	PPAS-MOL: 177827, 141000000
25	39.5	74.5	327	1	PPAS-MOL: 177827, 141000000
26	39.5	74.5	327	1	PPAS-MOL: 177827, 141000000
27	39.5	74.5	327	1	PPAS-MOL: 177827, 141000000
28	39.5	74.5	327	1	PPAS-MOL: 177827, 141000000
29	39.5	74.5	327	1	PPAS-MOL: 177827, 141000000
30	39.5	74.5	327	1	PPAS-MOL: 177827, 141000000
31	39.5	74.5	327	1	PPAS-MOL: 177827, 141000000
32	39.5	74.5	327	1	PPAS-MOL: 177827, 141000000
33	39.5	74.5	327	1	PPAS-MOL: 177827, 141000000

ALL HITS

Result ID	Score	Query Match length DB	ID	SWMAP	Description
34	32	60.4	433	1	HISX-PROT: 177827, 141000000
35	32	60.4	433	1	HISX-PROT: 177827, 141000000
36	32	60.4	433	1	HISX-PROT: 177827, 141000000
37	32	60.4	433	1	HISX-PROT: 177827, 141000000
38	32	60.4	433	1	HISX-PROT: 177827, 141000000
39	32	60.4	433	1	HISX-PROT: 177827, 141000000
40	32	60.4	433	1	HISX-PROT: 177827, 141000000
41	32	60.4	433	1	HISX-PROT: 177827, 141000000
42	32	60.4	433	1	HISX-PROT: 177827, 141000000
43	32	60.4	433	1	HISX-PROT: 177827, 141000000
44	32	60.4	433	1	HISX-PROT: 177827, 141000000
45	32	60.4	433	1	HISX-PROT: 177827, 141000000

Result ID	Score	Query Match length DB	ID	SWMAP	Description
34	32	60.4	433	1	HISX-PROT: 177827, 141000000
35	32	60.4	433	1	HISX-PROT: 177827, 141000000
36	32	60.4	433	1	HISX-PROT: 177827, 141000000
37	32	60.4	433	1	HISX-PROT: 177827, 141000000
38	32	60.4	433	1	HISX-PROT: 177827, 141000000
39	32	60.4	433	1	HISX-PROT: 177827, 141000000
40	32	60.4	433	1	HISX-PROT: 177827, 141000000
41	32	60.4	433	1	HISX-PROT: 177827, 141000000
42	32	60.4	433	1	HISX-PROT: 177827, 141000000
43	32	60.4	433	1	HISX-PROT: 177827, 141000000
44	32	60.4	433	1	HISX-PROT: 177827, 141000000
45	32	60.4	433	1	HISX-PROT: 177827, 141000000

29 1. ABBREVIATION
30 2. TITLE
31 3. AUTHOR
32 4. JOURNAL
33 5. YEAR
34 6. VOLUME
35 7. PAGE
36 8. ISSN
37 9. DOI
38 10. ABSTRACT
39 11. KEYWORDS
40 12. SUMMARY
41 13. REFERENCES
42 14. COMMENTS
43 15. INDEXING
44 16. CITED BY
45 17. FULLTEXT
46 18. DOWNLOAD
47 19. PRINT
48 20. EMAIL
49 21. WEB
50 22. FTP
51 23. GATEWAY
52 24. SEARCH
53 25. FILTER
54 26. SORT
55 27. PAGES
56 28. FULLTEXT

57 1. ABBREVIATION

58 2. TITLE

59 3. AUTHOR

60 4. JOURNAL

61 5. YEAR

62 6. VOLUME

63 7. PAGE

64 8. ISSN

65 9. DOI

66 10. ABSTRACT

67 11. KEYWORDS

68 12. SUMMARY

69 13. REFERENCES

70 14. COMMENTS

71 15. INDEXING

72 16. CITED BY

73 17. FULLTEXT

74 18. DOWNLOAD

75 19. PRINT

76 20. EMAIL

77 21. WEB

78 22. FTP

79 23. GATEWAY

80 24. SEARCH

81 25. FILTER

82 26. SORT

83 27. PAGES

84 28. FULLTEXT

85 29. DOWNLOAD

86 30. PRINT

87 31. EMAIL

88 32. WEB

89 33. FTP

90 34. GATEWAY

91 35. SEARCH

92 36. FILTER

93 37. SORT

94 38. FULLTEXT

95 39. DOWNLOAD

96 40. PRINT

97 41. EMAIL

98 42. WEB

99 43. FTP

100 44. GATEWAY

101 45. SEARCH

102 46. FILTER

103 47. SORT

104 48. PAGES

105 49. FULLTEXT

106 50. DOWNLOAD

107 51. PRINT

108 52. EMAIL

109 53. WEB

110 54. FTP

111 55. GATEWAY

112 56. SEARCH

113 57. FILTER

114 58. SORT

115 59. PAGES

116 60. FULLTEXT

117 61. DOWNLOAD

118 62. PRINT

119 63. EMAIL

120 64. WEB

121 65. FTP

122 66. GATEWAY

123 67. SEARCH

124 68. FILTER

125 69. SORT

126 70. PAGES

127 71. FULLTEXT

128 72. DOWNLOAD

129 73. PRINT

130 74. EMAIL

131 75. WEB

132 76. FTP

133 77. GATEWAY

134 78. SEARCH

135 79. FILTER

136 80. SORT

137 81. PAGES

138 82. FULLTEXT

139 83. DOWNLOAD

140 84. PRINT

141 85. EMAIL

142 86. WEB

143 87. FTP

144 88. GATEWAY

145 89. SEARCH

146 90. FILTER

147 91. SORT

148 92. PAGES

149 93. FULLTEXT

150 94. DOWNLOAD

151 95. PRINT

152 96. EMAIL

153 97. WEB

154 98. FTP

155 99. GATEWAY

156 100. SEARCH

157 101. FILTER

158 102. SORT

159 103. PAGES

160 104. FULLTEXT

161 105. DOWNLOAD

162 106. PRINT

163 107. EMAIL

164 108. WEB

165 109. FTP

166 110. GATEWAY

167 111. SEARCH

FT TRANSIT 1 2 MITOCHONDRIAL (CYTOPLASMIC)
 FT CHAIN 2 285 STEROID-DEPENDENT ACUTE REGULATOR PROTEIN
 FT CONFLICT 75 H-2 (118 HEMATOLOGICAL)
 FT CONFLICT 99 E-2 (118 HEMATOLOGICAL)
 SQ SEQUENCE 285 AA: 31945 MW: 146501.11992215 (K0004)

Query Match 100.0% Score 5.0 BH 1. Length 285
 Best Local Similarity 100.0% Pr 0.00036
 Matches 9, Conservative 0, Mismatch 0, Indels 0, Dels 0

OY 1 ABBGTCMW 9
 DB 218 ABBGTCMW 226

RESULT 4
 STAR_HORSE STANDARD: PR1 38 AA
 AC 046689;
 DT 15-DEC-1998 (bel. 37, created)
 DT 15-DEC-1998 (bel. 37, last sequence update)
 DT 10-MAY-2000 (bel. 49, last annotation update)
 STEROID-DEPENDENT ACUTE REGULATOR PROTEIN (K0004)
 GN STAR

OS Equus caballus (Horse);
 OC Eukaryota; Metazoa; Chordata; Gradat; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus;
 OX NCBI_taxid:9796;

KN (1)
 RP SEQUENCE FROM N.A.
 RC TISSUE-Follicle;
 RX MEDLINE-9412149; PMID: 922792;
 RA Kerhan A., Boerboom D., Sirois J.
 RT Human chorionic gonadotropin induces cAMP increase regulation of
 RT steroidogenic acute regulatory (STAR) gene expression in theca
 RT theca interna and granulosa cells of ovine preovulatory follicles;
 RT Endocrinology 143:667-674(1999);

CC -1- FUNCTION: PLAYS A KEY ROLE IN STEROID HORMONE SYNTHESIS BY
 CC ENHANCING THE METABOLISM OF CHOLESTEROL INTO PREGNENOLONE.
 CC TRANSPORTER THAT BINDS TO AND TRANSPORTS CHOLESTEROL THROUGH THE
 CC INTERMEMBRANE SPACE OF THE MITOCHONDRION (PROBABLY).

CC -1- SIMILARITY: BELONGS TO THE STAR FAMILY

CC This SWISS-PROT entry is copyright 1999 and is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL database.
 CC The European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its copyright is acknowledged
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement with the EMBL database.
 CC or send an email to license@sb-til.ch

DR FMR1 AF011667; AF042704.1;
 DR FMR1 AF011666; AAC04703.1;
 DR InterPro: IPR000799;
 DR InterPro: IPR002913;
 DR Pfam: PF01852; START1.1;
 DR PRINTS: PR00078; STARPOTEN;
 KM Lipid-binding; lipid transport; transport; Steroidogenesis;
 KM Mitochondrion; Transit peptide;
 FT CHAIN 1 285 MITOCHONDRIAL (CYTOPLASMIC);
 FT TRANSIT 1 285 STEROID-DEPENDENT ACUTE REGULATOR PROTEIN;
 SQ SEQUENCE 285 AA: 31852 MW: 13942.270 (K0004)

Query Match 100.0% Score 5.0 BH 1. Length 285
 Best Local Similarity 100.0% Pr 0.00036
 Matches 9, Conservative 0, Mismatch 0, Indels 0, Dels 0

OY 1 ABBGTCMW 9
 DB 218 ABBGTCMW 226

RESULT 5
 STAR_HUMAN STANDARD: PR1 285 AA
 AC P49675; Q16196;
 DT 01-FEB-1996 (bel. 33, created)
 DT 01-FEB-1996 (bel. 33, last sequence update)
 DT 30-MAY-2000 (bel. 49, last annotation update)
 STEROID-DEPENDENT ACUTE REGULATOR PROTEIN (K0004)
 GN STAR

OS Homo sapiens (human);
 OC Eukaryota; Metazoa; Chordata; Gradat; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catartia; Inimutia; Homo;
 OX NCBI_taxid:9606;

KN (1)
 RP SEQUENCE FROM N.A.
 RC TISSUE-Adrenal Cortex;
 RX MEDLINE-95281540; PMID: 7761409;
 RA Sawamura T., Holt J.A., Distel L.J., Strauss J.F., III, Lin D.
 RA Miller W.L., Palmiter R.D., Soto J.C., Soto J.C., Clark R.J.
 RA Stocco D.M.;
 RT Human steroidogenic acute regulatory (STAR) gene: full-length activity in
 RT Cos-1 cells, tissue-specific expression, and mapping of the
 RT structural gene to 8p11.2 and a pseudogene to chromosome 13;
 RT Proc. Natl. Acad. Sci. U.S.A. 92:4772-4776(1995);

KN (2)
 RP SEQUENCE FROM N.A.
 RC TISSUE-Placenta;
 RX MEDLINE-9604208; PMID: 7547990;
 RA Sawamura T., Lin D., Holt J.A., Miller W.L., Strauss J.F., III;
 RA Strauss J.F., III;
 RT Site of the human steroidogenic acute regulatory (STAR) gene: full-length activity in
 RT activity;
 RT Biochemistry 34:12506-12512(1995);

KN (3)
 RP SEQUENCE FROM N.A.
 RC TISSUE-Placenta;
 RX MEDLINE-9604208; PMID: 7547990;
 RA Sawamura T., Lin D., Holt J.A., Miller W.L., Strauss J.F., III;
 RA Strauss J.F., III;
 RT Site of the human steroidogenic acute regulatory (STAR) gene: full-length activity in
 RT activity;
 RT Biochemistry 34:12506-12512(1995);

KN (4)
 RP SEQUENCE FROM N.A.
 RC TISSUE-Brain;
 RA Yu W., Sarquiss J., Gibbs R.A.;
 RT Stimulated (N.W. 1997) by the EMBL/GenBank/Trinity databases;
 RT [5]
 RP VAF:AF011667; AF042704.1;
 RX MEDLINE-97066837; PMID: 8948662;
 RA Rose H.S., Sawamura T., Strauss J.F., III, Miller W.L.;
 RA "The pathophysiology and genetics of congenital lipid adrenal
 RA hyperplasia";

KN (5)
 RP VAF:AF011667; AF042704.1;
 RX MEDLINE-97066837; PMID: 8948662;
 RA Rose H.S., Sawamura T., Strauss J.F., III, Miller W.L.;
 RA "The pathophysiology and genetics of congenital lipid adrenal
 RA hyperplasia";
 KN (6)
 RP VAF:AF011667; AF042704.1;
 RX MEDLINE-97066837; PMID: 8948662;
 RA Rose H.S., Sawamura T., Strauss J.F., III, Miller W.L.;
 RA "The pathophysiology and genetics of congenital lipid adrenal
 RA hyperplasia";

CC -1- FUNCTION: PLAYS A KEY ROLE IN STEROID HORMONE SYNTHESIS BY
 CC ENHANCING THE METABOLISM OF CHOLESTEROL INTO PREGNENOLONE.
 CC TRANSPORTER THAT BINDS TO AND TRANSPORTS CHOLESTEROL THROUGH THE
 CC INTERMEMBRANE SPACE OF THE MITOCHONDRION (PROBABLY).

CC -1- SUBCELLULAR LOCATION: MITOCHONDRIAL
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN OVARIAN, ADRENAL CORTEX AND
 CC KIDNEY.
 CC 1- TRANSACT. INTERACT. IN STAR GENE EXPRESSION. SEE CH. ADRENAL

PA Strittman N., White H.E., Emshery ... W.D.P., Pappas M.B.,
 RA Blondell T.L.:
 RT "Comparative analyses of pentaxin: interactions for protein-
 assembly and ligand binding".
 RL Structure 2:1017-1027(1994).
 CC -1- FUNCTION: MIGHT SERVE THE ROLE OF "PROTEOLIPIDS".
 CC -1- SUBUNIT: HOMOPENTAMER. PENTAXIN (OR PENTAXIN) HAVE A DISULFIDE
 CC ARRANGEMENT OF 5 NONCOVALENTLY BOUND SUBUNITS.
 CC -1- SIMILARITY: BELONGS TO THE PENTAXIN FAMILY.
 CC
 CC This SWISS-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation
 CC the European Bioinformatics Institute, here are no restrictions on its
 CC use by non-profit institutions as long as its content is not to be
 CC modified and this statement is not removed, usage by and for commercial
 CC entities requires a license agreement (see http://www.ebi.ac.uk/Ensembl/
 CC or send an email to license@ebi.ac.uk)
 CC
 CC DR EMBL: M14026; AAA28270.1;
 DR PIR: G25192; G25192;
 DR PIR: G25193; G25193;
 DR PDB: 1LIM; 1S-OC1-95;
 DR InterPro: IPR001759;
 DR Pfam: PF00354; pentaxin: 1;
 DR PRINTS: PR00895; PENTAXIN;
 DR PROSITE: PS00289; PENTAXIN, 1;
 KW Pentaxin: Calcium; Glycoprotein; Signal; Post-translational
 FT SIGNAL 1 24
 FT CHAIN 25 242 G-RE/7140 (PENTAXIN 1.1)
 FT DOMAIN 25 242 PENTAXIN
 FT DISULFID 62 125
 FT DISULFID 112 144
 FT DISULFID 207 241
 FT CARBOHYD 147 147
 FT DOMAIN 52 67
 FT DOMAIN 59 60
 FT BINDING 63 63
 FT
 FT BINDING 63 63
 FT
 FT SIMILAR 139 153
 FT SEQUENCE 242 AA; 25773 MW; A521092 AHHH92 GRG64;
 N-LINKED (GLYCAN)
 BINDING: 2-DEHYDROXY-2-AMINO-3-PHOSPHATE-GLUTAMATE (PENTAXIN).
 INTERACTION WITH PHOSPHATE GROUP OF
 PHOSPHATE-GLUTAMATE (PENTAXIN).
 QUATERNARY AMMONIUM GROUP OF
 PHOSPHATE-GLUTAMATE (PENTAXIN).
 STRONG WITH CA-BINDING SITE-HIGH SUGARIN.

Query Match 66.08; Score: 31 D8 v2 Length: 242;
 Best Local Similarity 100.0%; Prel. Neg. 7;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 3 RGPIC 7
 DB 5 RGPIC 9

Search completed: August 22, 2001, 14:00:00
 Job time: 411 sec



A:Accession: PC7107
 A:Cross-references: DDBJ|AB018440
 A:Experimental source: strain KSM-2337
 A:Molecule type: protein
 A:Residues: 31-50 (HA2)
 C:Comment: This enzyme is a thermotaxin
 C:Keywords: hydrolase; glycosidase
 C:Name: Bgl-237

Query Match	92.1%	Score of 16.4	Length 821
Best local Similarity	83.3%	Pred. No. 1	
Matches	5	Conservative	1
		Mismatches	0
		Indels	0
		Gaps	0

QY	1	NOFCSWK	6
DB	204	NEFWWK	209

RESULT B
JC4815
[redacted] ovidogenic acute regulatory protein [redacted]
[redacted] species: Bos primigenius taurus (cattle)
[redacted] Date: 09 Nov 1997 [redacted] modified on: 16 Feb 2000

C:Accession: J04315
 F:Marling, S.; Post, W.; Falwiler, M.; Wolf, R.
 Biochem. Biophys. Res. Commun. 215, 64-65, 1995.
 A:Title: Molecular cloning and *in vivo* expression of the bovine arterial smooth muscle α -actin.
 X:Reference number: J04315; MUID:96011427

A:Accession: J04315
A:Molecule type: mRNA
A:Residues: 1-285 (EAA)
C:Comment: This protein is an acute controller of the rate-limiting step of cholesterol biosynthesis.
C:Genetics:
A:Gene: SLAV
E:226-264/region: metalloprotease-1-like inhibitor similarity.

[illegible]

Chemical protein BH1905 (imported - 04/11/15) halodurans (strain 6145)
 protein: bap11153.faln00000
 UniProt: Q1-Dec-2009 #sequence_revision: 10 #2-00 #text_changed: false

C::Accession: E83875
C::Takami, H., Nakaseko, K., Takai, Y. & Morita, M. Sasaki, T. & Minamide, N. & Ueda, T. & Hirose, A. (1990) Purification and characterization of the endonuclease III from *Mycobacterium tuberculosis* H37Rv. *Nucleic Acids Res.* 18, 4317-4331, 2006.
A::Title: Complete genome sequence of the obligate intracellular bacterium *Mycobacterium tuberculosis* H37Rv and its relationship to other mycobacterial genomes.
A::Reference number: A83650; M01D:2026.314
A::Accession: E83875
A::Status: preliminary
A::Molecule type: DNA
A::Residues: 1433<S>0
A::Cross-references: db:AB001519; db:BAC001; db:EMBL017445; db:ECHO0124; db:EST0080000
A::Experimental source: strain C-126
C::Genetics:
C::Gene: BH1805

```

Query Match:      86.8%  Score  7  DB  Z:  Length 434:
Best Local Similarity: 100.0%  P-Val
Matches  5/  Conserved  0/  Mismatch 4/35  Indels  0/
07      1 NUCBOW 5

```

11111
475 NOECW 37'

RESULT 10
 SE4304
 hypothetical protein YNP016_0102 (Saccharomyces cerevisiae)
 N:Alternative names: hypothetical protein ym14
 O:Species: Saccharomyces cerevisiae
 C:Date: 17 May 1996 #sequence_revision: 17 May 1996 #first_release: 29 Oct 1995
 C:Accession: S64304
 R:Rieder, M.; Mueller, A.; S. Brackner, M.; V. J. M.
 submitted to the Protein Sequence Database, May 1996
 A:reference number: S64071

A:Accession: S04104
 A:Reference type: RNA
 A:Residues: 1-620 (100%)
 A:Cross reference: EMBL:522730, N1:AF269759, F100424, Gen: F103473, E76761, D5P08:0N0004
 A:Experimental source: Strain: S2480
 C:Comments:
 A:Gene: M1P5.YG0012
 A:Map position: 7k

	Q7	Q8	Q9	Q10	Q11	Q12	Q13	Q14	Q15	Q16	Q17	Q18	Q19	Q20	Q21	Q22	Q23	Q24	Q25	Q26	Q27	Q28	Q29	Q30	Q31	Q32	Q33	Q34	Q35	Q36	Q37	Q38	Q39	Q40	Q41	Q42	Q43	Q44	Q45	Q46	Q47	Q48	Q49	Q50	Q51	Q52	Q53	Q54	Q55	Q56	Q57	Q58	Q59	Q60	Q61	Q62	Q63	Q64	Q65	Q66	Q67	Q68	Q69	Q70	Q71	Q72	Q73	Q74	Q75	Q76	Q77	Q78	Q79	Q80	Q81	Q82	Q83	Q84	Q85	Q86	Q87	Q88	Q89	Q90	Q91	Q92	Q93	Q94	Q95	Q96	Q97	Q98	Q99	Q100						
Q7	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
Q8	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
Q9	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
Q10	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100

RESULT 11

K Burton, J.
 submitted to the EMBL Data Library, accession 1925
 A: Accession number: J1901
 A: Accession: T2804
 A: Status: preliminary; translated 1-Jan-93(Exp-74043)
 A: Molecule type: tRNA
 A: Residues: 1-522; MW 12

A:Cross-references: EMBL:56698; PIR: P01397; J: J05161;IND0207; cESP:M365.3
 A:Experimental source: clone M195
 C:Gene:IGF
 A:Gene:IGF:M195
 A:Map position: 2
 A:Intermap: 195:1601-1602:1603:1604:1605:1606:1607:1608:1609:1610:1611:1612:1613:1614:1615:1616:1617:1618:1619:1620:1621:1622:1623:1624:1625:1626:1627:1628:1629:1630:1631:1632:1633:1634:1635:1636:1637:1638:1639:1640:1641:1642:1643:1644:1645:1646:1647:1648:1649:1650:1651:1652:1653:1654:1655:1656:1657:1658:1659:1660:1661:1662:1663:1664:1665:1666:1667:1668:1669:1670:1671:1672:1673:1674:1675:1676:1677:1678:1679:1680:1681:1682:1683:1684:1685:1686:1687:1688:1689:1690:1691:1692:1693:1694:1695:1696:1697:1698:1699:1700:1701:1702:1703:1704:1705:1706:1707:1708:1709:1710:1711:1712:1713:1714:1715:1716:1717:1718:1719:1720:1721:1722:1723:1724:1725:1726:1727:1728:1729:1730:1731:1732:1733:1734:1735:1736:1737:1738:1739:1740:1741:1742:1743:1744:1745:1746:1747:1748:1749:1750:1751:1752:1753:1754:1755:1756:1757:1758:1759:1760:1761:1762:1763:1764:1765:1766:1767:1768:1769:1770:1771:1772:1773:1774:1775:1776:1777:1778:1779:1780:1781:1782:1783:1784:1785:1786:1787:1788:1789:1790:1791:1792:1793:1794:1795:1796:1797:1798:1799:1800:1801:1802:1803:1804:1805:1806:1807:1808:1809:1810:1811:1812:1813:1814:1815:1816:1817:1818:1819:1820:1821:1822:1823:1824:1825:1826:1827:1828:1829:1830:1831:1832:1833:1834:1835:1836:1837:1838:1839:1840:1841:1842:1843:1844:1845:1846:1847:1848:1849:1850:1851:1852:1853:1854:1855:1856:1857:1858:1859:1860:1861:1862:1863:1864:1865:1866:1867:1868:1869:1870:1871:1872:1873:1874:1875:1876:1877:1878:1879:1880:1881:1882:1883:1884:1885:1886:1887:1888:1889:1890:1891:1892:1893:1894:1895:1896:1897:1898:1899:1900:1901:1902:1903:1904:1905:1906:1907:1908:1909:1910:1911:1912:1913:1914:1915:1916:1917:1918:1919:1920:1921:1922:1923:1924:1925:1926:1927:1928:1929:1930:1931:1932:1933:1934:1935:1936:1937:1938:1939:1940:1941:1942:1943:1944:1945:1946:1947:1948:1949:1950:1951:1952:1953:1954:1955:1956:1957:1958:1959:1960:1961:1962:1963:1964:1965:1966:1967:1968:1969:1970:1971:1972:1973:1974:1975:1976:1977:1978:1979:1980:1981:1982:1983:1984:1985:1986:1987:1988:1989:1990:1991:1992:1993:1994:1995:1996:1997:1998:1999:2000:2001:2002:2003:2004:2005:2006:2007:2008:2009:2010:2011:2012:2013:2014:2015:2016:2017:2018:2019:2020:2021:2022:2023:2024:2025:2026:2027:2028:2029:2030:2031:2032:2033:2034:2035:2036:2037:2038:2039:2040:2041:2042:2043:2044:2045:2046:2047:2048:2049:2050:2051:2052:2053:2054:2055:2056:2057:2058:2059:2060:2061:2062:2063:2064:2065:2066:2067:2068:2069:2070:2071:2072:2073:2074:2075:2076:2077:2078:2079:2080:2081:2082:2083:2084:2085:2086:2087:2088:2089:2090:2091:2092:2093:2094:2095:2096:2097:2098:2099:2100:2101:2102:2103:2104:2105:2106:2107:2108:2109:2110:2111:2112:2113:2114:2115:2116:2117:2118:2119:2120:2121:2122:2123:2124:2125:2126:2127:2128:2129:2130:2131:2132:2133:2134:2135:2136:2137:2138:2139:2140:2141:2142:2143:2144:2145:2146:2147:2148:2149:2150:2151:2152:2153:2154:2155:2156:2157:2158:2159:2160:2161:2162:2163:2164:2165:2166:2167:2168:2169:2170:2171:2172:2173:2174:2175:2176:2177:2178:2179:2180:2181:2182:2183:2184:2185:2186:2187:2188:2189:2190:2191:2192:2193:2194:2195:2196:2197:2198:2199:2200:2201:2202:2203:2204:2205:2206:2207:2208:2209:2210:2211:2212:2213:2214:2215:2216:2217:2218:2219:2220:2221:2222:2223:2224:2225:2226:2227:2228:2229:2230:2231:2232:2233:2234:2235:2236:2237:2238:2239:2240:2241:2242:2243:2244:2245:2246:2247:2248:2249:2250:2251:2252:2253:2254:2255:2256:2257:2258:2259:2260:2261:2262:2263:2264:2265:2266:2267:2268:2269:2270:2271:2272:2273:2274:2275:2276:2277:2278:2279:2280:2281:2282:2283:2284:2285:2286:2287:2288:2289:2290:2291:2292:2293:2294:2295:2296:2297:2298:2299:2300:2301:2302:2303:2304:2305:2306:2307:2308:2309:2310:2311:2312:2313:2314:2315:2316:2317:2318:2319:2320:2321:2322:2323:2324:2325:2326:2327:2328:2329:2330:2331:2332:2333:2334:2335:2336:2337:2338:2339:2340:2341:2342:2343:2344:2345:2346:2347:2348:2349:2350:2351:2352:2353:2354:2355:2356:2357:2358:2359:2360:2361:2362:2363:2364:2365:2366:2367:2368:2369:2370:2371:2372:2373:2374:2375:2376:2377:2378:2379:2380:2381:2382:2383:2384:2385:2386:2387:2388:2389:2390:2391:2392:2393:2394:2395:2396:

Query Match:	95.9%	Size: 117	bits: 6.22
Best Local Similarity	100.00%	Free: No. 1	20.0%
Matches	57	Conservative	0
		Missed	0
		Gap	0
CY	1	NCBI	5
	11111		
1b	127	NCBI	141
RESULT	12		
140486			
surfactin synthetase component 11 - <i>Bacillus subtilis</i> .			
NCBI term: name: 8.1.1.111 in synthetase 11 (Aa) surfactin synthetase/competence protein			
NCBI term: actin amino acid 11486 (37.34.2.1)			
C Species: <i>Bacillus subtilis</i>			
C Date: 12 Aug 1996			
C Accession: 14390, 360866, 569710, 410643, 345518, 325678, 354996			
C Cosmid: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 118, 119, 120, 121, 122, 123, 124, 125, 126, 127, 128, 129, 130, 131, 132, 133, 134, 135, 136, 137, 138, 139, 140, 141, 142, 143, 144, 145, 146, 147, 148, 149, 150, 151, 152, 153, 154, 155, 156, 157, 158, 159, 160, 161, 162, 163, 164, 165, 166, 167, 168, 169, 170, 171, 172, 173, 174, 175, 176, 177, 178, 179, 180, 181, 182, 183, 184, 185, 186, 187, 188, 189, 190, 191, 192, 193, 194, 195, 196, 197, 198, 199, 200, 201, 202, 203, 204, 205, 206, 207, 208, 209, 210, 211, 212, 213, 214, 215, 216, 217, 218, 219, 220, 221, 222, 223, 224, 225, 226, 227, 228, 229, 230, 231, 232, 233, 234, 235, 236, 237, 238, 239, 240, 241, 242, 243, 244, 245, 246, 247, 248, 249, 250, 251, 252, 253, 254, 255, 256, 257, 258, 259, 260, 261, 262, 263, 264, 265, 266, 267, 268, 269, 270, 271, 272, 273, 274, 275, 276, 277, 278, 279, 280, 281, 282, 283, 284, 285, 286, 287, 288, 289, 290, 291, 292, 293, 294, 295, 296, 297, 298, 299, 300, 301, 302, 303, 304, 305, 306, 307, 308, 309, 310, 311, 312, 313, 314, 315, 316, 317, 318, 319, 320, 321, 322, 323, 324, 325, 326, 327, 328, 329, 330, 331, 332, 333, 334, 335, 336, 337, 338, 339, 340, 341, 342, 343, 344, 345, 346, 347, 348, 349, 350, 351, 352, 353, 354, 355, 356, 357, 358, 359, 360, 361, 362, 363, 364, 365, 366, 367, 368, 369, 370, 371, 372, 373, 374, 375, 376, 377, 378, 379, 380, 381, 382, 383, 384, 385, 386, 387, 388, 389, 390, 391, 392, 393, 394, 395, 396, 397, 398, 399, 400, 401, 402, 403, 404, 405, 406, 407, 408, 409, 410, 411, 412, 413, 414, 415, 416, 417, 418, 419, 420, 421, 422, 423, 424, 425, 426, 427, 428, 429, 430, 431, 432, 433, 434, 435, 436, 437, 438, 439, 440, 441, 442, 443, 444, 445, 446, 447, 448, 449, 450, 451, 452, 453, 454, 455, 456, 457, 458, 459, 460, 461, 462, 463, 464, 465, 466, 467, 468, 469, 470, 471, 472, 473, 474, 475, 476, 477, 478, 479, 480, 481, 482, 483, 484, 485, 486, 487, 488, 489, 490, 491, 492, 493, 494, 495, 496, 497, 498, 499, 500, 501, 502, 503, 504, 505, 506, 507, 508, 509, 510, 511, 512, 513, 514, 515, 516, 517, 518, 519, 520, 521, 522, 523, 524, 525, 526, 527, 528, 529, 530, 531, 532, 533, 534, 535, 536, 537, 538, 539, 540, 541, 542, 543, 544, 545, 546, 547, 548, 549, 550, 551, 552, 553, 554, 555, 556, 557, 558, 559, 560, 561, 562, 563, 564, 565, 566, 567, 568, 569, 570, 571, 572, 573, 574, 575, 576, 577, 578, 579, 580, 581, 582, 583, 584, 585, 586, 587, 588, 589, 590, 591, 592, 593, 594, 595, 596, 597, 598, 599, 600, 601, 602, 603, 604, 605, 606, 607, 608, 609, 610, 611, 612, 613, 614, 615, 616, 617, 618, 619, 620, 621, 622, 623, 624, 625, 626, 627, 628, 629, 630, 631, 632, 633, 634, 635, 636, 637, 638, 639, 640, 641, 642, 643, 644, 645, 646, 647, 648, 649, 650, 651, 652, 653, 654, 655, 656, 657, 658, 659, 660, 661, 662, 663, 664, 665, 666, 667, 668, 669, 670, 671, 672, 673, 674, 675, 676, 677, 678, 679, 680, 681, 682, 683, 684, 685, 686, 687, 688, 689, 690, 691, 692, 693, 694, 695, 696, 697, 698, 699, 700, 701, 702, 703, 704, 705, 706, 707, 708,			

RESULT

STAR MUST

STAR MUST

STAR MUST

STAR MUST

STAR MUST

STAR MUST

STAR MUST

STAR MUST

STAR MUST

STAR MUST

STAR MUST

STAR MUST

STAR MUST

STAR MUST

STAR MUST

STAR MUST

STAR MUST

STAR MUST

STAR MUST

STAR MUST

STAR MUST

STAR MUST

STAR MUST

STAR MUST

STAR MUST

STAR MUST

STAR MUST

STAR MUST

STAR MUST

STAR MUST

STAR MUST

STAR MUST

STAR MUST

STAR MUST

STAR MUST

STAR MUST

STAR MUST

STAR MUST

STAR MUST

STAR MUST

STAR MUST

STAR MUST

STAR MUST

STAR MUST

STAR MUST

STAR MUST

STAR MUST

STAR MUST

STAR MUST

STAR MUST

STAR MUST

STAR MUST

STAR MUST

STAR MUST

STAR MUST

STAR MUST

STAR MUST

STAR MUST

STAR MUST

STAR MUST

STAR MUST

STAR MUST

STAR MUST

STAR MUST

STAR MUST

STAR MUST

STAR MUST

STAR MUST

STAR MUST

STAR MUST

STAR MUST

STAR MUST

STAR MUST

STAR MUST

STAR MUST

STAR MUST

STAR MUST

DR EMBL: AF201334: AAF09585.1: -
KM Microtubules: GTP-binding.
FT NP_BIND 148 154 GTP (XENopus A.).
SQ SEQUENCE 475 AA: 52931 MW: 38671.666AFAF80 CCK644

Query Match 100.0% Score 100.0 Length 176
Best Local Similarity 100.0% Prod. No. 422
Matches 63 Conservative 0 Mismatches 0 Indels 0 Gaps 0

UY 1 NOEWK 6
DB 476 NOEWK 381

RESULT 8
ID 25A1_RAT STANDARD: PRT 55 AA
AC Q05961:
DT 01-FEB-1994 (Ref. 28, Created)
DT 01-FEB-1994 (Ref. 28, Last annotated 4 Feb)
DE 15-DEC-1998 (Ref. 37, Last annotated 4 Feb)
PE (2-5') (110-ADENYLATE SYNTHETASE) (EC 2.7.7.7) ((XENopus A.).
SYNTHETASE 1) (2-5A SYNTHETASE 1)
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciuridae; Muridae; Murinae; Rattus

NCBI_Taxid:10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 94376704; PubMed 7744002;
RA Trive E.; Aspinall A.; Honkaniemi J.; Liska R.; Mello K.; Hassel A.;
Torti T.H.; Koles M.; Seppanen M.; Sirtanen M.;
RT "Transgenic potato plants expressing human 2'-5' oligonucleotide
synthetase are protected from potato virus X infection under field
conditions.";
RT Biotechnology 11:1048-1052(1993).
CC -1- CATALYTIC ACTIVITY: BINDS DOUBLE STRANDED RNA AND POLYMERIZES ADP
INTO PPpA(2'5'A)N OLIGOMERS, WHICH ACTIVATES THE LATERAL BRANCH
THAT, WHEN ACTIVATED, CLEAVES STRAND-STRAND BRANCHES.
CC -1- INDUCTION: BY INTERFERONS.
CC -1- SIMILARITY: BELONGS TO THE 2-5A SYNTHETASE FAMILY.
CC THIS SWISS-PROT entry is copyrighted. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation
at the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by any other party
without the EMBL/EBI authority is prohibited. For more information, please
or send an email to license@ebi.ac.uk.

EMBL: Z18877: CAA79317.1: -
DR PIR: S31407: S31407.
DR InterPro: IPR001797: -
DR PROSITE: PS00832: 25A_SYNTH_1: 1
DR PROSITE: PS00833: 25A_SYNTH_2: 1
KM RNA-binding: Transferase Nucleoside; Interase;
KM Interferon induction: MultiGene Family;
SQ SEQUENCE 358 AA: 41666 MW: A.0F.4.9: AS145MFA CCK644

Query Match 92.1% Score 59.9 DB 1: Length 358
Best Local Similarity 83.4% Prod. No. 122
Matches 5 Conservative 1 Mismatches 0 Indels 0 Gaps 0

UY 1 NOEWK 6
DB 314 NOEWK 319

RESULT 9
OAS1_RAT STANDARD: PRT 314 AA
ID OAS1_RAT

AC Q05961:
DT 01-FEB-1994 (Ref. 28, Created)
DT 01-FEB-1994 (Ref. 28, Last annotated 4 Feb)
DT 01-OCT-2000 (Ref. 40, Last annotated 4 Oct)
DE 2'-5'-OLIGONUCLEOTIDE SYNTHETASE 1 (EC 2.7.7.7) ((XENopus A.).
SYNTHETASE 1) (2-5A SYNTHETASE 1)
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciuridae; Muridae; Murinae; Rattus

NCBI_Taxid:10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 94376704; PubMed 7744002;
RA Trive E.; Aspinall A.; Honkaniemi J.; Liska R.; Mello K.; Hassel A.;
Torti T.H.; Koles M.; Seppanen M.; Sirtanen M.;
RT "Transgenic potato plants expressing human 2'-5' oligonucleotide
synthetase are protected from potato virus X infection under field
conditions.";
RT Biotechnology 11:1048-1052(1993).
CC -1- INDUCTION: BY INTERFERONS.
CC -1- SIMILARITY: BELONGS TO THE 2-5A SYNTHETASE FAMILY.
CC THIS SWISS-PROT entry is copyrighted. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation
at the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by any other party
without the EMBL/EBI authority is prohibited. For more information, please
or send an email to license@ebi.ac.uk.

EMBL: Z18877: CAA79317.1: -
DR PIR: S31407: S31407.
DR InterPro: IPR001797: -
DR PROSITE: PS00832: 25A_SYNTH_1: 1
DR PROSITE: PS00833: 25A_SYNTH_2: 1
DR PROSITE: PS00834: 25A_SYNTH_3: 1
KM RNA-binding: Transferase Nucleoside; Interase;
KM Interferon induction: MultiGene Family;
SQ SEQUENCE 358 AA: 41666 MW: A.0F.4.9: AS145MFA CCK644

Query Match 92.1% Score 59.9 DB 1: Length 358
Best Local Similarity 83.4% Prod. No. 122
Matches 5 Conservative 1 Mismatches 0 Indels 0 Gaps 0

UY 1 NOEWK 6
DB 314 NOEWK 319

RESULT 10
LVS1_SCHPO STANDARD: PRT 314 AA
ID LVS1_SCHPO
AC Q09644: Q09644.
DT 01-NOV-1995 (Ref. 42, Created)
DT 01-OCT-2000 (Ref. 40, Last annotated 4 Oct)
DT 01-OCT-2000 (Ref. 40, Last annotated 4 Oct)
DE SANGHARATNE JEWELRY GEMSTONE (RAT).
SYNTHETASE 1 (EC 2.7.7.7) ((XENopus A.).
SYNTHETASE 1) (2-5A SYNTHETASE 1)
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Basidiomycota;
OC Schizosaccharomycetes; Schizosaccharomycetaceae;
OC Schizosaccharomyces;
OC NCBI_Taxid 4896;
RN [1]
RP SEQUENCE FROM N.A.
ID STRAIN 9727

Matches 5: Conservative 0: Mutations 1: Indels 0: Gaps

Oy 1 NOBGMK 6

11111

Db 3084 NOBGMK 3089

Search completed: August 22, 2001, 14:30:57
Job time: 411 sec



DE SECRETED PROTEIN UNIT7 (FRAGMENT).
 GN WNT7.
 OS Branchiostoma belcheri.
 CC Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomida;
 CC Branchiostoma.
 DX NCBI_TaxID=7741;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Yasui K., Saiga H., Uemura M., Senba T.
 RT "Early body formation and expression of genes encoding
 RT secreted proteins, BbMP2/4, BbMP2/4 related in Branchiostoma
 RL submitted (Nov-1999) to the EMBL/GenBank/DDBJ databases
 CC -1- FUNCTION: PROBABLE DEVELOPMENTAL PROTEIN. MAY BE A SIGNALING
 CC MOLECULE WHICH AFFECT THE DEVELOPMENT OF DISCRETE REGIONS OF
 CC TISSUES. IS LIKELY TO SIGNAL OVER ONLY FIVE CELL DIAMETERS (BY
 CC SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: POSSIBLY SECRETED AND ASSOCIATES WITH THE
 CC EXTRACELLULAR MATRIX (BY SIMILARITY).
 CC -1- SIMILARITY: TO OTHER MEMBERS OF THE WNT FAMILY.
 DR EMBL: AF206449; AAF19839.1;
 DR InterPro: IPR000970;
 DR InterPro: IPR001781;
 DR Pfam: PF00110; Wnt: 1;
 DR ProDom: PD000094; 1;
 DR PROSITE: PS00246; WNT1; 1.
 DR SMART: SM0097; WNT1; 1.
 KW developmental protein; glycoprotein
 FT NONTER
 SQ SEQUENCE 244 AA; 27942 MW; 05590A1F22A9; 39974.

Query Match 86.8% Score 100.00 Length 244
 Best Local Similarity 83.3% Prod. No. 3002
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0

QY 1 NCBIW 6
 DB 40 NCBIW 45

RESULT 7
 Q9D609 PRELIMINARY; PRT; 201 AA.
 AC Q9D609;
 DT 01-MAR-2001 (EMBLrel. 16, Created)
 DT 01-MAR-2001 (EMBLrel. 16, Last sequence update)
 DI 01-MAR-2001 (EMBLrel. 16, Last annotation update)
 DE STROPHOMECIN ACUTE REGULATORY PROTEIN
 GN STAR.
 OS Gallus gallus (Chicken).
 CC Eukaryota; Metazoa; Chordata; Cephalochordata; Eudystemia;
 CC Archosauria; Aves; Neognathae; Galliformes; Chondestidae; Chondestes;
 CC Gallus.
 DX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA PubMed:11064158;
 RA Bauer M.P., Bridgman J.T., Langman J.M., Johnson A.L., Gaudz P.W.
 RT "Conservation of steroidogenic acute regulatory (STAR) protein
 RT structure and expression in vertebrates."
 RL Mol. Cell. Endocrinol. 168:119-125(2000).
 DR EMBL: AF220435; AAC28594.1;
 DR EMBL: AF220435; AAC28594.1;
 DR EMBL: AF220435; AAC28594.1;
 SQ SEQUENCE 281 AA; 31036 MW; 3663161G09A47; 39764.

Query Match 86.8% Score 100.00 Length 281
 Best Local Similarity 83.3% Prod. No. 12002
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0

QY 1 NCBIW 5
 DB 92 NCBIW 97

RESULT 8
 Q9C6D0 PRELIMINARY; PRT; 285 AA.
 AC Q9C6D0;
 DT 01-MAR-2001 (EMBLrel. 16, Created)
 DT 01-MAR-2001 (EMBLrel. 16, Last sequence update)
 DI 01-MAR-2001 (EMBLrel. 16, Last annotation update)
 DE STROPHOMECIN ACUTE REGULATORY PROTEIN
 GN STAR.
 OS Ovis aries (sheep).
 CC Eukaryota; Metazoa; Chordata; Cephalochordata; Eudystemia;
 CC Mammalia; Euarchontata; Artiodactyla; Cetartiodactyla; Bovidae; Bovinae;
 CC Bovidae; Caprinae; Ovis.
 DX NCBI_TaxID=9940;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA West L.A., Horvat R.D., Roess J.A., Porteus H.S., Bridgman J.T.
 RA Niswender G.D.
 RT "Steroidogenic Acute Regulatory Protein and Protein-Related
 RT Bromodiazepine Receptor Association of the Mitochondrial Membrane."
 RL Submitted (Jan-2000) to the EMBL/GenBank/DDBJ databases.
 DR EMBL: AF20292; AAC02464.1;
 DR EMBL: AF20292; AAC02464.1;
 SQ SEQUENCE 285 AA; 31895 MW; AB0101A1F295; 39644.

Query Match 86.8% Score 100.00 Length 347
 Best Local Similarity 83.3% Prod. No. 15002
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 1 NCBIW 6
 DB 92 NCBIW 97

RESULT 9
 Q61700 PRELIMINARY; PRT; 347 AA.
 AC Q61700;
 DI 01-AUG-1998 (EMBLrel. 07, Created)
 DI 01-AUG-1998 (EMBLrel. 07, Last sequence update)
 DI 01-MAR-2001 (EMBLrel. 16, Last annotation update)
 DE AMB1WNT7.
 GN WNT7B.
 OS Branchiostoma floridae (Florida lancelet) (Amphioxus).
 CC Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomida;
 CC Branchiostoma.
 DX NCBI_TaxID=7739;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Schubert M., Holland L.Z., De Robertis E., Johnson A.L.,
 RL Schubert M. (Apr 1999) to the EMBL/GenBank/DDBJ databases.
 CC -1- FUNCTION: PROBABLE DEVELOPMENTAL PROTEIN. MAY BE A SIGNALING
 CC MOLECULE WHICH AFFECT THE DEVELOPMENT OF DISCRETE REGIONS OF
 CC TISSUES. IS LIKELY TO SIGNAL OVER ONLY FIVE CELL DIAMETERS (BY
 CC SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: POSSIBLY SECRETED AND ASSOCIATES WITH THE
 CC EXTRACELLULAR MATRIX.
 CC -1- SIMILARITY: TO OTHER MEMBERS OF THE WNT FAMILY.
 DR EMBL: AF061975; AAC60434.1;
 DR InterPro: IPR000970;
 DR Pfam: PF00110; Wnt: 1;
 DR PROSITE: PS00246; WNT1; 1.
 DR SMART: SM0097; WNT1; 1.
 KW developmental protein; glycoprotein
 SQ SEQUENCE 347 AA; 39425 MW; A607390740647; 39944.

CC for designing oligonucleotides for sequencing and identifying
CC antigenic determinants of STAR protein
XX
SO Sequence 14 AA:

Query Match 100.0%; Score 54; Pos 17; Length 14;
Best Local Similarity 100.0%; Prod No. 0475;
Matches 9; Conservation 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AEHGPTCMV 9
DB 1 aehgptcmv 9

RESULT 4
AAW13238
ID AAW13238 standard; Protein: 284 AA;
AC AAW13238;

21-MAY-1997 (first entry)

Human steroidogenesis acute regulatory protein mutant delta Arg272;
Human; steroidogenesis; acute regulatory protein; STAR; analysis;
mutation; detection; prenatal; genetic defect; congenital; protein;
lipoid adrenal hyperplasia; treatment; prevention; gene
replacement therapy; hypochloremic salt wasting; mutant.

Homo sapiens.

W09629348-A1.

26-SEP-1996.

22-MAR-1996; 94WD-US03896.

23-MAR-1995; 95US-0410540.

(REGC) UNIV CALIFORNIA.

(UTPR) UNIV PENNSYLVANIA.

Lin D, Miller WJ, Strauss JF;

WPI: 1996 443330/44.

Isolated human steroidogenesis acute regulatory protein gene used
for detection of mutation(s) of this gene that cause congenital
lipoid adrenal hyperplasia

Claim 16; Page 7; 89pp; English.

The present sequence is the human steroidogenesis acute regulatory
protein (STAR), congenital lipoid adrenal hyperplasia (GLAH)
associated mutant, delta Arg272 (delta Arg272). The delta Arg272
mutant is associated with the STAR gene for such a mutation is
useful in the detection (e.g., prenatal) of CAH associated
genetic defects or its transmission to children. CAH can be
treated by protein or gene replacement therapy, which can also be
used to prevent or treat hyperchloremic hyponatremia.

Sequence 284 AA:

Query Match 100.0%; Score 54; Pos 17; Length 284;
Best Local Similarity 100.0%; Prod No. 0475;
Matches 9; Conservation 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AEHGPTCMV 9
DB 218 aehgptcmv 226

RESULT 5
AAW74153
ID AAW74153 standard; Protein: 284 AA;
AC AAW74153;

05-MAY-1999 (first entry)

Mouse steroidogenic acute regulatory protein.

STAR; steroidogenesis; acute regulatory protein; Mouse; McNamee; Albright syndrome;
steroid hormone dependent disorder; adrenal; hyperplasia; congenital; LCAH;
lipoid congenital adrenal hyperplasia; infertility; sexual maturation;
androgen-responsive tumours; hypoadrenalism; therapy; progesterone level.

Mus sp.

US8972240-A.

16-FEB-1999.

04-MAY-1999; 95US-0548960.

04-MAY-1999; 95US-0548960.

(UTPR) UNIV TEXAS TECH HEALTH SCI CTR.

Clark RJ, Stocco DM;

WPI: 1999 16720714.

N-PSDB; AAX18169, AAX18170.

New nucleic acid encoding steroidogenesis acute regulatory protein
useful for treatment of steroid hormone dependent disorders such as
lipoid congenital adrenal hyperplasia, infertility and
androgen responsive tumours

Claim 1; Column 37-38, 25pp; Engl. 1999.

This sequence is the steroidogenesis acute regulatory protein (STAR)
of the invention. The STAR coding sequence and its products or
derivatives may be used as probes and primers for PCR hybridisation
studies and in the treatment of steroid hormone dependent disorders such
as lipoid congenital adrenal hyperplasia (LCAH), infertility, sexual
maturation, androgen-responsive tumours, hypoadrenalism, and hypogonadism.

McNamee AL; Albright syndrome; adrenal hyperplasia congenita; and hypogonadism.
McNamee AL; Albright syndrome; adrenal hyperplasia congenita; and hypogonadism.
and so a risk of spontaneous abortion.

Sequence 284 AA:

Query Match 100.0%; Score 54; Pos 20; Length 284;
Best Local Similarity 100.0%; Prod No. 0475;
Matches 9; Conservation 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AEHGPTCMV 9
DB 217 aehgptcmv 225

RESULT 6

AAV72841
ID AAV72841 standard; Protein: 284 AA

AAV72841;

31-MAY-2001 (first entry)

Mouse steroidogenic acute regulatory protein (STAR)

Mouse; steroidogenesis; acute regulatory protein; STAR

QY 1 AEGPTGCV 9
 |||||
 Db 218 aegptgcv 225

RESULT 8
 ID AAM00814
 AC AAM00814 standard: Protein: 285 AA.
 XX
 AC AAM00814:
 XX
 DT 21-MAY-1997 (first entry)
 XX
 DE Human steroidogenesis acute regulator, protein.
 XX
 KM Human; steroidogenesis; acute regulatory protein hstAR; analysis;
 KM mutation; detection; prenatal; neonatal; congenital; protein;
 KM lipid adrenal hyperplasia; treatment; prevention; gene;
 KM replacement therapy; hypercholesterolemia.
 XX
 OS Homo sapiens.

Key Location/Qualifiers
 Region 5
 FT /note "potential site for protein kinase C mediated phosphorylation"
 FT 13
 FT /note "potential site for protein kinase C mediated phosphorylation"
 FT 56..57
 FT /note "potential site for protein kinase A mediated phosphorylation"
 FT 100
 FT /note "potential site for protein kinase A mediated phosphorylation"
 FT 110
 FT /note "potential site for protein kinase A mediated phosphorylation"
 FT 186
 FT /note "potential site for protein kinase A mediated phosphorylation"
 FT 195..196
 FT /note "potential site for protein kinase A mediated phosphorylation"
 FT 277
 FT /note "potential site for protein kinase A mediated phosphorylation"
 FT Region
 FT W09629348-A1
 XX
 PN 26-SEP-1996.
 XX
 PF 22-MAR-1996: 96W00803896.
 XX
 PR 23-MAR-1995: 950S-0410540.
 XX
 PA (REGC) UNIV CALIFORNIA.
 PA (DYPE) UNIV PENNSYLVANIA.
 XX
 PI Lin D, Miller ML, Strauss JF:
 XX
 DR WPI: 1996-44340/44.
 DR N-PSDB: AAT3650.
 XX
 PT Isolated human steroidogenesis acute regulatory protein gene - used
 PT for detection of mutation(s) of this gene that cause congenital
 PT lipid adrenal hyperplasia
 XX
 PS Claim 1; Pages 62-63; 89pp; English.
 XX
 CC The present sequence is the human steroidogenesis acute
 CC regulatory protein (hstAR). The hstAR gene can be analyzed for
 CC mutations to detect (a) a prenatal diagnosis of congenital

CC with congenital lipid adrenal hyperplasia (CAH) or its
 CC transmission to children. CAH can be treated by prenatal or gene
 CC replacement therapy, which can be used to prevent or treat
 CC hypercholesterolemia.
 CC A human adrenal cortex cDNA library was screened with a mouse hstAR
 CC probe to isolate a 1.6 kb insert. The coding region of the
 CC residue protein. When it was cloned into pSP61 and expressed in
 CC COS-1 cells co-transfected with pCMVcat and pBLXcat, it increased the
 CC level of pregnenolone synthesis from 0.1 to 1.0 fold.
 CC 20 alpha-hydroxycholesterol.
 XX
 SU Sequence 285 AA

Query Match 100.0% Score 549 98.1% Pos 285
 Best Local Similarity 100.0% Pos 285
 Matches 99 238944100 0% Mismatches 0% Gaps 0%

QY 1 AEGPTGCV 9
 |||||
 Db 218 aegptgcv 225

RESULT 9
 ID AAM13233
 AC AAM13233 standard: Protein: 285 AA.
 XX
 AC AAM13233:
 XX
 DT 21 MAY 1997 (first entry)
 XX
 DE Human steroidogenesis acute regulator, protein hstAR; analysis;
 XX
 KM Human; steroidogenesis; acute regulatory protein hstAR; analysis;
 KM mutation; detection; prenatal; neonatal; congenital; protein;
 KM lipid adrenal hyperplasia; treatment; prevention; gene;
 KM replacement therapy; hypercholesterolemia.
 XX
 OS Homo sapiens.

Key Location/Qualifiers
 Region 169
 FT /note "wild type is substituted with G17"
 FT W09629348-A1
 XX
 PN 26-SEP-1996.
 XX
 PF 22-MAR-1996: 96W00803896.
 XX
 PR 23-MAR-1995: 950S-0410540.
 XX
 PA (REGC) UNIV CALIFORNIA.
 PA (DYPE) UNIV PENNSYLVANIA.
 XX
 PI Lin D, Miller ML, Strauss JF:
 XX
 DR WPI: 1996-44340/44.
 DR N-PSDB: AAT3650.
 XX
 PT Isolated human steroidogenesis acute regulatory protein gene - used
 PT for detection of mutation(s) of this gene that cause congenital
 PT lipid adrenal hyperplasia
 XX
 PS Claim 13; Page 7; 89pp; English.
 XX
 CC The present sequence is the human steroidogenesis acute regulatory
 CC protein (hstAR). Congenital lipid adrenal hyperplasia (CAH)
 CC associated mutant, glutamyl. Analysis of the hstAR gene for such a
 CC mutation is useful in the detection of (a) prenatal diagnosis of CAH
 CC associated mutant, or (b) a transmission to children. CAH
 CC can be treated by prenatal or gene replacement therapy, which can
 CC also be used to prevent or treat hypercholesterolemia.

XX DE Human steroidogenic acute regulatory (STAR) protein.
 XX KM Human; steroidogenic acute regulatory protein STAR;
 KM gene therapy; steroid hormone-dependent disorder; LCH;
 KM lipid congenital adrenal hyperplasia; sexual maturation;
 KM infertility; androgen responsive tumor; precocious puberty;
 KM hypoadrenalism; hypoadrenalism; McCune-Albright syndrome;
 KM adrenal-hypoplasia congenita; cytochrome.
 XX OS Homo sapiens.
 XX FH Key Location/Qualifiers
 FT Misc-difference 156 /note "Encoded by CM: this feature corresponds
 FT to the translation exception for the sequence shown
 FT in (AAD02909)."
 FT Modified-site 54..60 /note "PKA phosphorylation site"
 FT Modified-site 58..69 /note "CK phosphorylation site"
 FT Modified-site 195 /note "PKA phosphorylation site"
 FT Modified-site 233..234 /note "PKA phosphorylation site"
 FT Modified-site 238 /note "PKC phosphorylation site"
 FT Modified-site 277 /note "PKA phosphorylation site"
 XX PN US619455-B1
 XX PD 27-FEB-2001.
 XX PE 07-JUN-1996: 960S-0659254.
 XX PR 04-NOV-1995: 950S-0538950.
 XX PA (BYTE-) UNIV TEXAS TECH HEALTH SCI CTR.
 XX PI Stocco DM, Clark RJ;
 XX DR WPL: 2001-217936/22;
 XX NM N-PSDB: AAD02909, AAD02912.
 XX PT Novel nucleic acid encoding steroidogenic acute regulatory protein,
 XX PT useful for treating steroid hormone-dependent disorders.
 XX PS Example 14: Fig 5; 41pp; English.
 XX CC The invention relates to steroidogenic acute regulatory protein
 CC (STAR) and nucleic acid molecules encoding them. STAR proteins
 CC are used for regulating steroidogenesis. More particularly, these
 CC proteins are involved in regulating cholesterol transport into
 CC the mitochondria of a cell. The nucleic acid molecules of the
 CC invention are useful in gene therapy for the treatment of steroid
 CC hormone-dependent disorders, particularly lipid congenital
 CC adrenal hyperplasia (LCH), infertility, sexual maturation,
 CC androgen-responsive tumors, precocious puberty, McCune-Albright
 CC syndrome, adrenal-hypoplasia congenita or hypoadrenalism.
 CC hypoadrenalism. They are also useful for ex vivo gene
 CC of the steroidogenic acute regulatory protein.
 CC The present sequence is human steroidogenic acute regulatory
 CC protein (STAR).
 XX CC
 XX Sequence 285 AA;

Query Match 100.0%; Score 44.1422; Length 285;
 Best Local Similarity 100.0%; Prod. N. 1.075;
 Matches 9; Conservative 0; Mismatch 0; Indels 0; Gaps 0;
 QY 1 AENRPGMV 9

DB 218 actaprim 225
 |||||

RESULT 14
 ID AAM13246
 AC AAM13246;
 XX 21-MAY 1997 (first entry)
 XX DE Human steroidogenic acute regulatory protein mutant Ala218Val.
 XX KM Human; steroidogenesis; acute adren. hyp. prot. def. LCH; analysis;
 KM mutation; detection; prenatal; androgen responsive tumor;
 KM lipid congenital adrenal hyperplasia; treatment; cytochrome;
 KM replacement therapy; hypoadrenalism; cytochrome.
 XX OS Homo sapiens.
 XX FH Key Location/Qualifiers
 FT Misc-difference 218 /note "Wild type: Ala substituted with Val"
 FT W09629438-A1.
 FT 26-SEP 1996.
 XX PD 26-SEP 1996.
 XX PR 22-MAR-1996: 96WO-0804936.
 XX PR 23-MAR-1995: 96US-6410940.
 XX PA (REG-) UNIV CALIFORNIA,
 XX PA (TYPE-) UNIV PENNSYLVANIA.
 XX PI Lin D, Miller WL, Strauss JF;
 XX DR WPL: 1996-4410944.
 XX NM N-PSDB: AAM13246.
 XX PT Isolated human steroidogenesis acute regulatory protein gene used
 XX PT for detection of mutant (s) of this gene that cause congenital
 XX PT lipid adrenal hyperplasia
 XX PS Claim 13; Page 7; 8pp; English.
 XX CC The present sequence is the human steroidogenic acute regulatory
 XX CC protein (STAR), congenital lipid congenital hyperplasia (LCH)
 XX CC associated mutant, Ala218Val. Analysis of the STAR gene for such a
 XX CC mutation is useful in the detection of congenital (s) of STAR
 XX CC associated genetic defects, or in a substitution to children, LCH
 XX CC can be treated by protein or gene replacement therapy, which can
 XX CC also be used to prevent or treat hypoadrenalism.
 XX CC
 XX Sequence 285 AA;

Query Match 92.5%; Score 14.1422; Length 285;
 Best Local Similarity 100.0%; Prod. N. 0.67;
 Matches 9; Conservative 0; Mismatch 0; Indels 0; Gaps 0;
 QY 2 ENRPGMV 9
 |||||
 DB 219 cbpimv 226

RESULT 14
 AAM13356
 ID AAM13356 Standard; protein; 300 AA;
 XX AAM13356;
 XX AC AAM13356;



SEQUENCE CHARACTERISTICS:
 LENGTH: 14 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-659-254-3

Query Match 100.0% Score 5.00 DB 1.0 Length 14
 Best Local Similarity 100.0% Pred. No. 10147
 Matches 9; Conservative 0; Mismatches 0; Indels 0

OY 1 AHHPTCMV 9
 11111111
 DB 1 AHHPTCMV 9

RESULT 5
 US-08-659-254-2
 Sequence 2, Application US/0865925;
 Patent No. 619455

GENERAL INFORMATION:
 APPLICANT: Storco, Douglas M.
 APPLICANT: Clark, Dr. Barbara J.
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR REGULATION
 TITLE OF INVENTION: OF STRANDEDNESS
 NUMBER OF SEQUENCES: 19
 CORRESPONDENCE ADDRESS:
 ADDRESS: Akin Gump, Strauss, Hays & Field, L.P.
 STREET: 1900 Frost Bank Plaza, 9th Floor, Suite 900
 CITY: Austin
 STATE: TX
 COUNTRY: U.S.A.
 ZIP: 78701

COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.00
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/659,254
 FILING DATE: 07-JUN-1996
 CLASSIFICATION: 530
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/09,739,967
 FILING DATE: 04-OCT-1995

ATTORNEY/AGENT INFORMATION:
 NAME: Mayfield, Denise L.
 REGISTRATION NUMBER: 33,742
 REFERENCE/DOCKET NUMBER: 43376,0006
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 512/499-6296
 TELEFAX: 512/499-6290

INFORMATION FOR SEQ ID NO: 7:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 276 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-659-254-2

Query Match 100.0% Score 5.00 DB 1.0 Length 276
 Best Local Similarity 100.0% Pred. No. 0.027
 Matches 9; Conservative 0; Mismatches 0; Indels 0

OY 1 AHHPTCMV 9
 11111111
 DB 217 AHHPTCMV 2.5

RESULT 6
 US-08-538-960-2
 Sequence 2, Application US/08548960
 Patent No. 5672280

GENERAL INFORMATION:
 APPLICANT: Storco, Douglas M.
 APPLICANT: Clark, Barbara J.
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
 TITLE OF INVENTION: REGULATION OF STRANDEDNESS
 NUMBER OF SEQUENCES: 14
 CORRESPONDENCE ADDRESS:
 ADDRESS: Akin Gump, Strauss, Hays & Field, L.P.
 STREET: 1900 Frost Bank Plaza, 9th Floor, Suite 900
 CITY: Austin
 STATE: TX
 COUNTRY: U.S.A.
 ZIP: 78701

COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 COMPUTER: IBM PC compatible
 SOFTWARE: Patent Release #1.0, Version #1.00
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: 07/04,534,961
 FILING DATE: 09-OCT-1995
 CLASSIFICATION: 530
 ATTORNEY/AGENT INFORMATION:
 NAME: Mayfield, Denise L.
 REGISTRATION NUMBER: 33,742
 REFERENCE/DOCKET NUMBER: 43376,0006
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 512/499-6296
 TELEFAX: 512/499-6290

INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 284 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-538-960-2

Query Match 100.0% Score 5.00 DB 2.5 Length 284
 Best Local Similarity 100.0% Pred. No. 0.028
 Matches 9; Conservative 0; Mismatches 0; Indels 0

OY 1 AHHPTCMV 9
 11111111
 DB 217 AHHPTCMV 2.5

RESULT 7
 US-08-410-540-2
 Sequence 2, Application US/08410540
 Patent No. 5806744

GENERAL INFORMATION:
 APPLICANT: Miller, Walter L.
 APPLICANT: Lin, Dong
 TITLE OF INVENTION: IDENTIFICATION OF HEPATITIS B
 TITLE OF INVENTION: ASSOCIATED WITH CHRONIC HEPATITIS B
 NUMBER OF SEQUENCES: 30
 CORRESPONDENCE ADDRESS:
 ADDRESS: 6000 Redwood Crest, Houston, TX 77056
 STREET: 6000 Redwood Crest
 CITY: Houston, TX
 STATE: TX
 COUNTRY: US
 ZIP: 77056

COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 COMPUTER: IBM PC compatible

TITLE OF INVENTION: Therapeutic And Diagnostic Methods
TITLE OF INVENTION: Acid Composition And Method For Determining Acid
NUMBER OF INVENTIONS: 21
CORRESPONDENCE ADDRESS:
ADDRESS: Pennine & Edmunds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC DOS/MS DOS
SOFTWARE: Patent Release #1.4, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/659-254-7
FILING DATE: 25-JUN-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mistrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/INVENT NUMBER: 7426-015
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
TELEFAX: 212 8698864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 2556 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-659-254-20

Query Match 56.0% Score 3 : 16 17 Length 2556
Best Local Similarity 100.0% Pctd. No 17-02
Matches 5: Conservative 0: Mismatches 0: Indels 0: Gaps 0

OY 3 BHPIC 7
DB 171 BHPIC 175

RESULT 11
US-08-532 384 20
Sequence 20, Application US/08532381
Patent No. 6083904
GENERAL INFORMATION:
APPLICANT: Aftavakis-Tsakonas, S. et al.
TITLE OF INVENTION: Therapeutic And Diagnostic Methods
TITLE OF INVENTION: Acid Composition And Method For Determining Acid
NUMBER OF INVENTIONS: 21
CORRESPONDENCE ADDRESS:
ADDRESS: Pennine & Edmunds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC DOS/MS DOS
SOFTWARE: Patent Release #1.4, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08-532-384
FILING DATE:
CLASSIFICATION: 424

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/084,599
FILING DATE: 25-JUN-1993
APPLICANT/AGENT INFORMATION:
NAME: Mistrock, S. Leslie
REGISTRATION NUMBER: 18,872
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
TELEFAX: 212 8698864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 2556 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-542-484-20

Query Match 66.0% Score 3 : 16 17 Length 2556
Best Local Similarity 100.0% Pctd. No 17-02
Matches 5: Conservative 0: Mismatches 0: Indels 0: Gaps 0

OY 3 BHPIC 7
DB 171 BHPIC 175

RESULT 12
US-08-173-5108 40
Sequence 40, Application US/08135108
Patent No. 5747290
GENERAL INFORMATION:
APPLICANT: MATTHEW MOYLE ET AL.
TITLE OF INVENTION: NOVEL NEUTROPHIL INHIBITORS
NUMBER OF INVENTIONS: 104
CORRESPONDENCE ADDRESS:
ADDRESS: 1900 & 1900
STREET: 645 West Fifth Street
CITY: San Francisco
STATE: California
COUNTRY: U.S.A.
ZIP: 94071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 MB
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM PC, DOS 3.1
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08-173-5108
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/151,063
FILING DATE: 10-NOV-1993
APPLICATION NUMBER: 08/060,433
FILING DATE: 11-MAY-1993
APPLICATION NUMBER: 07/996,972
FILING DATE: 24-DEC-1992
APPLICATION NUMBER: 07/881,721
FILING DATE: 11-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: HILSON, SUZANNE L.
REGISTRATION NUMBER: 40,158
TELECOMMUNICATION INFORMATION:
TELEPHONE: (413) 489-1600
TELEFAX: (413) 955-0440
TELEX: 67-4510
INFORMATION FOR SEQ ID NO: 40:

RECORDING CHARGE: 1.00
 LINE: 1. AMIN: 1.00
 TYPE: 1. AMIN: 1.00
 MOD: 1.00
 MOD: 1.00

Copy: 1.00
 Host: 1.00
 Mod: 1.00
 Mod: 1.00

2. 1.00
 2. 1.00

2. 1.00

2. 1.00

2. 1.00

2. 1.00

2. 1.00

2. 1.00

2. 1.00

2. 1.00

2. 1.00

2. 1.00

2. 1.00

2. 1.00

2. 1.00

2. 1.00

2. 1.00

2. 1.00

2. 1.00

2. 1.00

2. 1.00

RECORDING CHARGE: 1.00
 LINE: 1. AMIN: 1.00
 TYPE: 1. AMIN: 1.00
 MOD: 1.00
 MOD: 1.00

Copy: 1.00
 Host: 1.00
 Mod: 1.00
 Mod: 1.00

2. 1.00
 2. 1.00

2. 1.00

2. 1.00

2. 1.00

2. 1.00

2. 1.00

2. 1.00

2. 1.00

2. 1.00

2. 1.00

2. 1.00

2. 1.00

2. 1.00

2. 1.00

2. 1.00

2. 1.00

2. 1.00

2. 1.00

2. 1.00

2. 1.00

GENERAL INFORMATION:

APPLICANT: WANG, Xun
APPLICANT: DUVICK, Jonathan P.
APPLICANT: BRIGGS, Steven P.
TITLE OF INVENTION: PCR BASED CDNA SUBSTITUTIVE CLONING
TITLE OF INVENTION: METHOD
NUMBER OF SEQUENCES: 39

CORRESPONDENCE ADDRESS:

ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0. Vols on #1.00
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/858,767

FILING DATE: 19-MAY-1997

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

PRIOR APPLICATION NUMBER: US 08/481,487

FILING DATE: 07-JUN-1995

ATTORNEY/AGENT INFORMATION:

NAME: BENT, Stephen A.

REGISTRATION NUMBER: 29,768

REFERENCE/DOCKET NUMBER: 3329/32977-B

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202)672-5300

TELEFAX: (202)672-5399

TELEX: 904136

INFORMATION FOR SEQ ID NO: 28:

SEQUENCE CHARACTERISTICS:

LENGTH: 99 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-858-767-28

Query Match

62.38; Score 3; DB 2; Length 99;

Best Local Similarity: 44.48; Freq. No. 13;

Matches: 4; Conservative: 4; Mismatches: 1; Indels: 0;

QY 1 AHHGPTCW 9

28 SENGPCVI 36

Search completed: August 22, 2001, 14:00:12
Job time: 366 sec



XX Sequence 12 AA:

Query Match 100.0%; Score 46.16; Length 12;
 Best Local Similarity 100.0%; Prod No. 41
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 1 NOEGRK 6
 |||||
 Db 7 upgawk 12

RESULT 4
 AAW72833
 ID AAW72833 standard; peptide: 12 AA.

AC AAW72833;
 XX
 DT 31 MAY 2001 (first entry)

XX Mouse trypsin peptide #25 for analysis of steroid hormone production

XX Mouse; steroidogenic acute regulatory protein (STAR);
 gene therapy; steroid hormone-dependent disorder; hAH;
 lipoid congenital adrenal hyperplasia; sexual maturation;
 infertility; androgen-responsive form; adrenocortical failure;
 hypogonadotropic hypogonadism; Mettune A bright syndrome;
 adrenal-hypoplasia congenita; cytosolic trypsin peptide

XX Mus SP.

OS 086194555-B1.

PN 27 FEB-2001.

PD 07-JUN-1996. 9608-0659254.

PE 04-NOV-1995. 9508-0538960.

PR (UNITE-) UNIV TEXAS TECH HEALTH SCI 7940.

PA Stocco DM, Clark HJ.

PI WPL: 2001-217925/22.

DR Novel nucleic acid encoding steroidogenic acute regulatory protein.

PT useful for treating steroid hormone-dependent disorders.

PS Example 2: Column 28; 41pp; English.

XX The invention relates to steroids and more particularly to proteins
 (STAR) and nucleic acid molecules encoding them. STAR proteins
 are used for regulating steroidogenesis. More particularly, these
 proteins are involved in regulating the steroid transport into
 the mitochondria of a cell. The role of acid molecules of the
 invention are useful in gene therapy for the treatment of steroid
 hormone dependent disorders, particularly, lipoid congenital
 adrenal hyperplasia (LCAH), infertility, sexual maturation,
 androgen-responsive tumors, precocious puberty, Mettune A-like
 syndrome, adrenal hypoplasia congenita or hypogonadotropic
 hypoadrenalism. They are also useful as a substrate for protein
 of the steroidogenic acute regulatory protein.
 CC The present sequence is trypsin peptide #25. This peptide is
 used in the cloning and sequence analysis of cDNA encoding the
 30kDa form of STAR protein. This peptide is also used in the
 analysis of the STAR protein sequence. Peptide #25 is useful
 CC for determining oligonucleotides for screening and identifying
 CC antigenic determinants of STAR protein.

XX Sequence 12 AA:

Query Match 100.0%; Score 46.16; Length 12;
 Best Local Similarity 100.0%; Prod No. 41
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 1 NOEGRK 6
 |||||
 Db 7 upgawk 12

RESULT 5
 AAW14246
 ID AAW14246 standard; Protein: 284 AA

AC AAW14246;
 XX

DT 21 MAY 1997 (first entry)

XX Human steroidogenesis acute regulatory protein (hSTAR);

XX human; steroidogenesis; acute regulatory protein; STAR; androgen-
 XX mutation; defect congenital; gonadal hypoplasia; protein;
 XX lipoid congenital hyperplasia; treatment; precocious puberty;
 XX replacement therapy; hypercortisolism; congenital; mutation;
 XX Homo sapiens.

OS W0629438 A1.

PN 26-SEP-1996.

PD 22-MAR-1996. 9608-0538960.

PE 23-MAR-1995. 9508-0410540.

PR (RSCG) UNIV CALIFORNIA.

PA (UNITE-) UNIV PENNSYLVANIA.

PI Liu D, Miller WL, Strauss JF.

PS WPL: 1996-441130/44.

DR Isolated human steroidogenesis acute regulatory protein gene used
 for detection of mutation(s) of the gene that cause congenital
 lipoid adrenal hyperplasia

PT claim 16; page 89pp; English.

PS The present sequence is the human steroidogenesis acute regulatory
 protein (hSTAR), congenital lipoid adrenal hyperplasia (CAH)
 associated mutant delta Arg272 (see also type residue Arg272 has
 CC been deleted). Analyzing the hSTAR sequence for such a mutation is
 CC useful in the detection (e.g., prenatal) of CAH associated
 CC genetic defects. or its transmission. The isolated hAH can be
 CC treated by protein or gene therapy. The therapy which can also be
 CC used to prevent or treat hypercortisolism.

XX Sequence 284 AA:

Query Match 100.0%; Score 46.16; Length 284;
 Best Local Similarity 100.0%; Prod No. 41
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 1 NOEGRK 6
 |||||
 Db 92 upgawk 97

RESULT 6
 AAW74153
 ID AAW74153 standard; protein: 284 AA

AC AAW74153;
 XX

DT 21 MAY 1997 (first entry)

XX Human steroidogenesis acute regulatory protein (hSTAR);

OS W0629438 A1.

PN 26-SEP-1996.

PD 22-MAR-1996. 9608-0538960.

Query Match 100.0%; Score 48; db 22; Length 255;
 Best Local Similarity 100.0%; Prod No 9.5;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0

UY 1 NOEGRK 6
 |||||
 DB 91 nqgwkk 96

RESULT 8

AAW13236
 ID AAW13236 standard; Protein: 285 AA

AC AAW13236;

XX 21-MAY-1997 (first entry)

DE Human steroidogenesis acute regulatory protein mutant Ala219Val.

XX Human steroidogenesis; acute regulatory protein; hSTAR analysis;

KW mutation; detection; prenatal; genetic defect; congenital; protein;

KW lipid adrenal hyperplasia; treatment; prevention; gene;

OS Homo sapiens.

XX Key Location/Qualifiers

FT Misc difference 218 /note "Wild type AAW13236 substituted with Val"

PN W09629338-A1.

PD 26-SEP-1996.

PF 22-MAR-1996; 96WD-0503896.

PR 23-MAR-1995; 95US-0410540.

PA (R03C) UNIV CALIFORNIA.

PA (TYPE) UNIV PENNSYLVANIA.

PI Lin D, Miller W, Strauss JF;

DR WPI: 1996-44130/44.

DR N-PSDB; AAT62021.

XX Isolated human steroidogenesis acute regulatory protein gene used

PT for detection of mutation(s) of this gene that cause congenital

PF lipid adrenal hyperplasia

CC Claim 13; Page : 89pp; English.

CC The present sequence is the human steroidogenesis acute regulatory

CC protein (hSTAR), congenital lipid adrenal hyperplasia (LAP)

CC associated mutant, Ala219Val. Analysis for the hSTAR gene for such a

CC mutation is useful in the detection of congenital adrenal hyperplasia

CC associated genetic defects, or its transmission to children. hAR

CC also be used to prevent or treat hypoadrenalism.

XX Sequence 285 AA;

Query Match 100.0%; Score 48; db 22; Length 255;

Best Local Similarity 100.0%; Prod No 9.5;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0

UY 1 NOEGRK 6

DB 92 nqgwkk 97

RESULT 9

AAW13237
 ID AAW13237 standard; Protein: 285 AA.

AC AAW13237;

XX 21-MAY-1997 (first entry)

DE Human steroidogenesis acute regulatory protein mutant Leu275Pro.

XX Human steroidogenesis; acute regulatory protein; hSTAR analysis;

KW mutation; detection; prenatal; genetic defect; congenital; protein;

KW lipid adrenal hyperplasia; treatment; prevention; gene;

OS Homo sapiens.

XX Key Location/Qualifiers

FT Misc difference 276 /note "Wild type AAW13237 substituted with Pro"

PN W09629338-A1.

PD 26-SEP-1996.

PF 22-MAR-1996; 96WD-0503896.

PR 23-MAR-1995; 95US-0410540.

PA (R03C) UNIV CALIFORNIA.

PA (TYPE) UNIV PENNSYLVANIA.

PI Lin D, Miller W, Strauss JF;

DR WPI: 1996-44130/44.

DR N-PSDB; AAT62022.

XX Isolated human steroidogenesis acute regulatory protein gene used

PT for detection of mutation(s) of this gene that cause congenital

PF lipid adrenal hyperplasia

CC Claim 13; Page : 89pp; English.

CC The present sequence is the human steroidogenesis acute regulatory

CC protein (hSTAR), congenital lipid adrenal hyperplasia (LAP)

CC associated mutant, Leu275Pro. Analysis for the hSTAR gene for such a

CC mutation is useful in the detection of congenital adrenal hyperplasia

CC associated genetic defects, or its transmission to children. hAR

CC also be used to prevent or treat hypoadrenalism.

XX Sequence 285 AA;

Query Match 100.0%; Score 48; db 22; Length 255;

Best Local Similarity 100.0%; Prod No 9.5;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0

UY 1 NOEGRK 6

DB 92 nqgwkk 97

RESULT 10

AAW00814
 ID AAW00814 standard; Protein: 285 AA

AC AAW00814;

XX 21-MAY-1997 (first entry)

DE Human steroidogenesis acute regulatory protein.

XX Human steroidogenesis; acute regulatory protein; hSTAR analysis;

XX AAW13234:
 XX
 XX
 DT 21-MAY-1997 (first entry)
 XX
 DE Human steroidogenesis acute regulatory protein mutant Arg182Leu.
 XX
 KW Human: steroidogenesis; acute regulatory protein; hSTAR analysis;
 KW mutation; detection; prenatal; genetic defect; congenital; protein;
 KW lipid adrenal hyperplasia; treatment; prevention; gene;
 KW replacement therapy; hypercholesterolemia infant.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 182
 FT Note: "Wild type Arg substituted with Leu"
 XX
 FN W06629348-A1.
 XX
 PD 26-SEP-1996.
 XX
 XX 22-MAR-1996; 96W0-0503876.
 XX
 XX 23-MAR-1995; 95DS-0410540.
 XX
 PA (REGC) UNIV CALIFORNIA.
 PA (TYPE) UNIV PENNSYLVANIA.
 XX
 PI Lin D, Miller WL, Strauss JF.
 XX
 DK WP1: 1996-44310/74.
 DR N-PSDB; AAF62019.
 XX
 PT Isolated human steroidogenesis acute regulatory protein gene - used
 PT for detection of mutation(s) of this gene that cause congenital
 PT lipid adrenal hyperplasia
 XX
 PS Claim 13: Page 7: 89pp; English.
 XX
 CC The present sequence is the human steroidogenesis acute regulatory
 CC protein (hSTAR), congenital lipid adrenal hyperplasia (CAH)
 CC associated mutant, Arg182Leu. Analysing the hSTAR gene for such a
 CC mutation is useful in the detection (e.g., prenatal) of CAH
 CC associated genetic defects, or the transmission to children. CAH
 CC can be treated by protein or gene replacement therapy, which can
 CC also be used to prevent or treat hypercholesterolemia.
 XX
 SO Sequence 285 AA.
 XX

Query Match 100.0%; Score 94; Lb 17; Length 285;
 Best Local Similarity 100.0%; Prot. N: 9, 5;
 Matches 5; Conservative 0; Mismatches 0; Inerts 0; Gaps 0

QY 1 NOESMK 6
 II III
 DB 92 nqesmk 97

RESULT 13
 AAW13235
 ID AAW13235 standard; Protein: 285 AA.
 XX
 AC AAW13235:
 XX
 DT 21-MAY-1997 (first entry)
 XX
 DE Human steroidogenesis acute regulatory protein mutant Glu174Gly.
 XX
 KW Human: steroidogenesis; acute regulatory protein; hSTAR analysis;
 KW mutation; detection; prenatal; genetic defect; congenital; protein;
 KW lipid adrenal hyperplasia; treatment; prevention; gene.

KW replacement therapy; hypercholesterolemia infant.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 169
 FT Note: "Wild type Glu substituted with Gly"
 XX
 FN W06629348-A1.
 XX
 PD 26-SEP-1996.
 XX
 XX 22-MAR-1996; 96W0-0503876.
 XX
 XX 23-MAR-1995; 95DS-0410540.
 XX
 PA (REGC) UNIV CALIFORNIA.
 PA (TYPE) UNIV PENNSYLVANIA.
 XX
 PI Lin D, Miller WL, Strauss JF.
 XX
 DK WP1: 1996-44310/74.
 DR N-PSDB; AAF62020.
 XX
 PT Isolated human steroidogenesis acute regulatory protein gene - used
 PT for detection of mutation(s) of this gene that cause congenital
 PT lipid adrenal hyperplasia
 XX
 PS Claim 13: Page 7: 89pp; English.
 XX
 CC The present sequence is the human steroidogenesis acute regulatory
 CC protein (hSTAR), congenital lipid adrenal hyperplasia (CAH)
 CC associated mutant, Glu174Gly. Analysing the hSTAR gene for such a
 CC mutation is useful in the detection (e.g., prenatal) of CAH
 CC associated genetic defects, or the transmission to children. CAH
 CC can be treated by protein or gene replacement therapy, which can
 CC also be used to prevent or treat hypercholesterolemia.
 XX
 SO Sequence 285 AA.
 XX

Query Match 100.0%; Score 93; Lb 17; Length 285;
 Best Local Similarity 100.0%; Prot. N: 9, 5;
 Matches 5; Conservative 0; Mismatches 0; Inerts 0; Gaps 0

QY 1 NOESMK 6
 II III
 DB 92 nqesmk 97

RESULT 14
 AAW72838
 ID AAW72838 standard; Protein: 285 AA.
 XX
 AC AAW72838:
 XX
 DT 31-MAY-2001 (first entry)
 XX
 DE Human steroidogenesis acute regulatory protein (STAR) protein.
 XX
 KW Human: steroidogenesis; acute regulatory protein; STAR;
 KW gene therapy; steroid hormone-dependent disorder (CAH);
 KW lipid congenital adrenal hyperplasia; genetic defect; mutation;
 KW infertility; androgen-responsive; mutant; prenatal; puberty;
 KW hypoadrenalism; hypoadrenalism; Met; to Adrenal syndrome;
 KW adrenal-hyperplasia congenital; cystic.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 156
 FT Note: "Encoded by 'A' this for an orthopods
 to the translated sequence from the cDNA shown



SEQUENCE CHARACTERISTICS:
 LENGTH: 11 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-659-254-8

Query Match 100.0%; Score 69; E-4; Length 11;
 Best Local Similarity 100.0%; Prev. No. 6241;
 Matches 6; Conservative 0; Mismatches 0; Gaps 0;

QY 1 N083WK 6
 DB 4 N083WK 9

RESULT 5
 US-08-538-960-4
 Sequence 4; Title: 11 Amino Acids;
 Patent No. 5872240

GENERAL INFORMATION:
 APPLICANT: Stocco, Douglas M.
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
 TITRATION OF AMINO ACIDS
 NUMBER OF SEQUENCES: 14
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: AKIN, Gump, Strauss, Gump & Field, L.L.P.
 STREET: 1900 Frost Bank Plaza, P.O. Box 6200
 CITY: Austin
 STATE: TX
 COUNTRY: U.S.A.
 ZIP: 78701
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/538,960
 FILING DATE: Concurrently Herein
 CLASSIFICATION: 530
 ATTORNEY/AGENT INFORMATION:
 NAME: Mayfield, Denise L.
 REGISTRATION NUMBER: 34,742
 REFERENCE/INCKET NUMBER: 43471, 04/2/201M
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 512/499-6290
 TELEFAX: 512/499-6290
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 12 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-538-960-4

Query Match 100.0%; Score 69; E-4; Length 12;
 Best Local Similarity 100.0%; Prev. No. 6241;
 Matches 6; Conservative 0; Mismatches 0; Gaps 0;

QY 1 N083WK 6
 DB 7 N083WK 12

RESULT 6
 US-08-659-254-4
 Sequence 4; Title: 11 Amino Acids;
 Patent No. 5872240

Patient No. 619455
 GENERAL INFORMATION:

APPLICANT: Stocco, Douglas M.
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR REGULATION
 NUMBER OF SEQUENCES: 19
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: AKIN, Gump, Strauss, Gump & Field, L.L.P.
 STREET: 1900 Frost Bank Plaza, P.O. Box 6200
 CITY: Austin
 STATE: TX
 COUNTRY: U.S.A.
 ZIP: 78701
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/659,254
 FILING DATE: 07-JUN-1996
 CLASSIFICATION: 530
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/538,960
 FILING DATE: 04-OCT-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Mayfield, Denise L.
 REGISTRATION NUMBER: 34,742
 REFERENCE/INCKET NUMBER: 43471, 04/2/201M
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 512/499-6290
 TELEFAX: 512/499-6290
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 12 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-659-254-4

Query Match 100.0%; Score 69; E-4; Length 12;
 Best Local Similarity 100.0%; Prev. No. 6241;
 Matches 6; Conservative 0; Mismatches 0; Gaps 0;

QY 1 N083WK 6
 DB 7 N083WK 12

RESULT 7
 US-08-659-254-2
 Sequence 2; Application US/08/659,254
 Patent No. 619455

GENERAL INFORMATION:
 APPLICANT: Stocco, Douglas M.
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR REGULATION
 NUMBER OF SEQUENCES: 19
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: AKIN, Gump, Strauss, Gump & Field, L.L.P.
 STREET: 1900 Frost Bank Plaza, P.O. Box 6200
 CITY: Austin
 STATE: TX
 COUNTRY: U.S.A.
 ZIP: 78701
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 SOFTWARE: Patent Release #1.0, Version #1.30

SOURCE: FBI/DOJ - Bureau of Prisons - Washington, DC
 CORRESPONDENCE: A
 APPLICATION NUMBER: 10000000000000000000
 FILING DATE: 07/10/00
 CLASSIFICATION: A
 PROGRAM APPLICATION: A
 APPLICATION NUMBER: 10000000000000000000
 FILING DATE: 07/10/00
 ATTORNEY/AGENT INFORMATION:
 NAME: MAYNARD, JAMES L.
 IDENTIFICATION NUMBER: 10000000000000000000
 REFERENCE/WORKSHEET NUMBER: 10000000000000000000
 FILING IDENTIFICATION NUMBER: 10000000000000000000
 TELEPHONE: 1-214-749-6200
 TELEFAX: 1-214-749-6200
 INFORMATION REPORT NUMBER: 10000000000000000000
 SIGNATURE: CHAVALIER, JAMES L.
 LENGTH: 20000000000000000000
 TYPE: 00000000000000000000
 STANDARDIZED: 00000000000000000000
 MODIFIED: 10000000000000000000
 US ON 6/29/2004 2

ENTRY MATCH: 10000000000000000000
 LOCAL LOSS: 10000000000000000000
 MATCHES: 10000000000000000000
 20 1 NUMBER: 10000000000000000000
 10 1 NUMBER: 10000000000000000000

REF: 10000000000000000000
 US ON 5/28/2004 2
 Sequence: 10000000000000000000
 Patent No.: 5872200
 GENERAL INFORMATION:
 APPLICANT: STANLEY, JAMES L.
 TITLE OF INVENTION: 10000000000000000000
 TITLE OF INVENTION: 10000000000000000000
 NUMBER OF SEQUENCES: 10000000000000000000
 ADDRESS: 10000000000000000000
 ADDRESS: 10000000000000000000
 STREET: 10000000000000000000
 CITY: 10000000000000000000
 STATE: 10000000000000000000
 COUNTRY: 10000000000000000000
 ZIP: 10000000000000000000
 COMPUTER RESEARCH: 10000000000000000000
 METHOD TYPE: 10000000000000000000
 COMPUTER: 10000000000000000000
 OPERATING SYSTEM: 10000000000000000000
 SOFTWARE: 10000000000000000000
 APPLICANT INFORMATION:
 APPLICANT NUMBER: 10000000000000000000
 FILING DATE: 10000000000000000000
 CLASSIFICATION: 10000000000000000000
 ATTORNEY/AGENT INFORMATION:
 NAME: MAYNARD, JAMES L.
 IDENTIFICATION NUMBER: 10000000000000000000
 REFERENCE/WORKSHEET NUMBER: 10000000000000000000
 FILING IDENTIFICATION NUMBER: 10000000000000000000
 TELEPHONE: 1-214-749-6200
 TELEFAX: 1-214-749-6200
 INFORMATION REPORT NUMBER: 10000000000000000000
 SIGNATURE: CHAVALIER, JAMES L.
 LENGTH: 20000000000000000000
 TYPE: 00000000000000000000
 STANDARDIZED: 00000000000000000000
 MODIFIED: 10000000000000000000
 US ON 6/29/2004 2

SOURCE: FBI/DOJ - Bureau of Prisons - Washington, DC
 CORRESPONDENCE: A
 APPLICATION NUMBER: 10000000000000000000
 FILING DATE: 07/10/00
 CLASSIFICATION: A
 PROGRAM APPLICATION: A
 APPLICATION NUMBER: 10000000000000000000
 FILING DATE: 07/10/00
 ATTORNEY/AGENT INFORMATION:
 NAME: MAYNARD, JAMES L.
 IDENTIFICATION NUMBER: 10000000000000000000
 REFERENCE/WORKSHEET NUMBER: 10000000000000000000
 FILING IDENTIFICATION NUMBER: 10000000000000000000
 TELEPHONE: 1-214-749-6200
 TELEFAX: 1-214-749-6200
 INFORMATION REPORT NUMBER: 10000000000000000000
 SIGNATURE: CHAVALIER, JAMES L.
 LENGTH: 20000000000000000000
 TYPE: 00000000000000000000
 STANDARDIZED: 00000000000000000000
 MODIFIED: 10000000000000000000
 US ON 6/29/2004 2

ENTRY MATCH: 10000000000000000000
 LOCAL LOSS: 10000000000000000000
 MATCHES: 10000000000000000000
 20 1 NUMBER: 10000000000000000000
 10 1 NUMBER: 10000000000000000000

REF: 10000000000000000000
 US ON 5/28/2004 2
 Sequence: 10000000000000000000
 Patent No.: 5872200
 GENERAL INFORMATION:
 APPLICANT: STANLEY, JAMES L.
 TITLE OF INVENTION: 10000000000000000000
 TITLE OF INVENTION: 10000000000000000000
 NUMBER OF SEQUENCES: 10000000000000000000
 ADDRESS: 10000000000000000000
 ADDRESS: 10000000000000000000
 STREET: 10000000000000000000
 CITY: 10000000000000000000
 STATE: 10000000000000000000
 COUNTRY: 10000000000000000000
 ZIP: 10000000000000000000
 COMPUTER RESEARCH: 10000000000000000000
 METHOD TYPE: 10000000000000000000
 COMPUTER: 10000000000000000000
 OPERATING SYSTEM: 10000000000000000000
 SOFTWARE: 10000000000000000000
 APPLICANT INFORMATION:
 APPLICANT NUMBER: 10000000000000000000
 FILING DATE: 10000000000000000000
 CLASSIFICATION: 10000000000000000000
 ATTORNEY/AGENT INFORMATION:
 NAME: MAYNARD, JAMES L.
 IDENTIFICATION NUMBER: 10000000000000000000
 REFERENCE/WORKSHEET NUMBER: 10000000000000000000
 FILING IDENTIFICATION NUMBER: 10000000000000000000
 TELEPHONE: 1-214-749-6200
 TELEFAX: 1-214-749-6200
 INFORMATION REPORT NUMBER: 10000000000000000000
 SIGNATURE: CHAVALIER, JAMES L.
 LENGTH: 20000000000000000000
 TYPE: 00000000000000000000
 STANDARDIZED: 00000000000000000000
 MODIFIED: 10000000000000000000
 US ON 6/29/2004 2

1111 OF INVENTION: COMPOSITIONS AND METHODS FOR REGULATION
 TITLE OF INVENTION: OF STENOPODEPISIN
 NUMBER OF SEQUENCES: 19
 CORRESPONDENCE ADDRESS:
 ADDRESS: Apts. 600, Streets, Box 5 Field, 11111
 STREET: 1900 Frost Bank Plaza, 91111 Express Avenue
 CITY: Austin
 STATE: TX
 COUNTRY: U.S.A.
 ZIP: 78701
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Vol 100 #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: 08/08/659,254
 FILING DATE: 07-JUN-1996
 CLASSIFICATION: 530
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 08/08/548,560
 FILING DATE: 04-OCT-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Mayfield, Denise L.
 REGISTRATION NUMBER: 33,732
 REFERENCE/DOCKET NUMBER: 4476, 000
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 512/469-6200
 TELEFAX: 512/499-6290
 INFORMATION FOR SEQ ID NO: 18:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 285 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 US-08-659-254-18

Query Match 100.0% Score 91.00 Length 285
 Best Local Similarity 100.0% Pct 91.00
 Matches 6: Conservative 0: Mismatches 0: Indels 0: Gaps 0

QY 1 NOEWMK 6
 111111
 DB 92 NOEWMK 97

RESULT 11
 US-08-361-920-21
 Sequence 21: Application US/08/44999
 Patent No. 5457046
 GENERAL INFORMATION:
 APPLICANT: Woelcke, Helge F.
 APPLICANT: Hagen, Frederick
 APPLICANT: Hjort, Carsten M.
 APPLICANT: Sven, Hestrup
 TITLE OF INVENTION: An Enzyme Capable of Regulating Cellulose
 NUMBER OF SEQUENCES: 85
 CORRESPONDENCE ADDRESS:
 ADDRESS: M. 5457046, N. 5457046, N. 5457046, N. 5457046
 STREET: 405 Lexington Avenue, 62nd Floor
 CITY: New York
 STATE: New York
 COUNTRY: United States of America
 ZIP: 10174-6201
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/661,520
 FILING DATE:

CLASSIFICATION: 435
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 07/941,803
 FILING DATE: 28-02-1992
 APPLICATION NUMBER: PK 1159760
 FILING DATE: 09-MAY-1990
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: PK/08/1/00 45
 FILING DATE: 08-MAY-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Lamb, Elias J.
 REGISTRATION NUMBER: 33,728
 REFERENCE/DOCKET NUMBER: 4433, 2, 75
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 212 967-0123
 TELEFAX: 212 967-0298
 INFORMATION FOR SEQ ID NO: 21:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 514 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-361-920-21

Query Match 86.8% Score 91.00 Length 514
 Best Local Similarity 83.4% Pct 91.00
 Matches 9: Conservative 0: Mismatches 1: Indels 0: Gaps 0

QY 1 NOEWMK 9
 111111
 DB 205 NOEWMK 210

RESULT 12
 US-08-479-939-21
 Sequence 21: Application US/08/479039
 Patent No. 5686593
 GENERAL INFORMATION:
 APPLICANT: Woelcke, Helge F.
 APPLICANT: Hagen, Frederick
 APPLICANT: Hjort, Carsten M.
 APPLICANT: Sven, Hestrup
 TITLE OF INVENTION: An Enzyme Capable of Regulating Cellulose
 NUMBER OF SEQUENCES: 85
 CORRESPONDENCE ADDRESS:
 ADDRESS: M. 5686593, N. 5686593, N. 5686593, N. 5686593
 STREET: 405 Lexington Avenue, 62nd Floor
 CITY: New York
 STATE: New York
 COUNTRY: United States of America
 ZIP: 10174-6201
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: 08/08/479,039
 FILING DATE: 07-JUN-1995
 CLASSIFICATION: 435
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US/08/461,000
 FILING DATE: 22-DEC-1994
 APPLICATION NUMBER: PK 115-770
 FILING DATE: 28-02-1992
 APPLICATION NUMBER: PK 115-770
 FILING DATE: 09-MAY-1990
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: PK/08/1/00 45
 FILING DATE: 08-MAY-1991
 ATTORNEY/AGENT INFORMATION:

NAME: LARRY...
 REFERENCE: N...
 TELEPHONE: ...
 TELEFAX: ...
 SPOUSAL CHAUVINITY: ...
 TYPE: ...
 MODIFIED: ...

DATE: ...
 TIME: ...
 LOCATION: ...

PERSON: ...
 ADDRESS: ...
 CITY: ...
 STATE: ...
 COUNTRY: ...

APPLICATION NUMBER: ...
 FILING DATE: ...
 APPLICATION NUMBER: ...
 FILING DATE: ...
 APPLICATION NUMBER: ...
 FILING DATE: ...

INFORMATION FOR ...
 LENGTH: ...
 TYPE: ...

NAME: ...
 REFERENCE: ...
 TELEPHONE: ...
 TELEFAX: ...
 SPOUSAL CHAUVINITY: ...
 TYPE: ...
 MODIFIED: ...

DATE: ...
 TIME: ...
 LOCATION: ...

PERSON: ...
 ADDRESS: ...
 CITY: ...
 STATE: ...
 COUNTRY: ...

APPLICATION NUMBER: ...
 FILING DATE: ...
 APPLICATION NUMBER: ...
 FILING DATE: ...
 APPLICATION NUMBER: ...
 FILING DATE: ...

INFORMATION FOR ...
 LENGTH: ...
 TYPE: ...

Matches 4: Conservative 2: Mismatches 0: Indels 0: Gaps 0

Job time: 366 sec

QY 1 NOGWR 6
1:11:
Db 26 NEEGWR 31

RESULT 15

US-08-373-215-12

Sequence 12, Application US/08/373215

Patent No. 5973110

GENERAL INFORMATION:

APPLICANT: Muller, Daniel

APPLICANT: Brownell, Elise

APPLICANT: Delaria, Katherine

TITLE OF INVENTION: Cytotoxic F-Like Cyste Antagonist as a

NUMBER OF SEQUENCES: 13

CORRESPONDENCE ADDRESS:

ADDRESSEE: Hannon & Allegretti, LLC

STREET: 10 S. Wacker Drive Suite 400

CITY: Chicago

STATE: IL

COUNTRY: USA

ZIP: 60606

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.40

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/373,215

FILING DATE: 18-MAY-1995

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: WO PCT/US95/00002

FILING DATE: 15-JUL-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/915,923

FILING DATE: 17-JUL-1992

ATTORNEY/AGENT INFORMATION:

NAME: McDonnell, John J

REGISTRATION NUMBER: 26,949

REFERENCE/DOCKET NUMBER: 93613 C

TELECOMMUNICATION INFORMATION:

TELEPHONE: (312) 715-1000

TELEFAX: (312) 715-1234

INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:

LENGTH: 96 amino acids

TYPE: amino acid

STRANDEDNESS: not relevant

TOPOLOGY: not relevant

MOLECULE TYPE: protein

FEATURE:

NAME/KEY: Protein

LOCATION: 1..96

OTHER INFORMATION: /note: "hucall"

US-08-373-215-12

Query Match 84.2% Score 52 LB 2: Length 96

Best Local Similarity 66.7% Proc. No. 32

Matches 4: Conservative 2: Mismatches 0: Indels 0: Gaps 0

QY 1 NOGWR 6
1:11:
Db 26 NEEGWR 31

Search completed: August 22, 2001, 14:40:12



06 Plasmid sym (pNC234).

06 Bacteria; Proteobacteria; alpha subphylum Rhizobium.

06 Rhizobiaceae, Rhizobium.



GenInfo version 1.5
Copyright (c) 1994-2000 Nucleon Ltd.

OM protein - protein search, using SW model

Run on: August 22, 2001, 14:27:21 Search time: 11:11.8 seconds
(41 hours of human's)

27121 Matches with e-value < 10

Title: US-08-659-254-5

Sequence: 1 GSTCVALAMATHHEMPED 19

Scoring table: MDSUM62

Gapop 10.0, Gapext 0.5

Searched: 425026 seqs, 142305027 positions

Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

- 1: SPTREMBL_16:*
- 2: SP_archaea:*
- 3: SP_bacteria:*
- 4: SP_fungi:*
- 5: SP_invertebrate:*
- 6: SP_mammal:*
- 7: SP_mhc:*
- 8: SP_organelle:*
- 9: SP_phage:*
- 10: SP_plant:*
- 11: SP_protist:*
- 12: SP_unclassified:*
- 13: SP_vertebrate:*
- 14: SP_virus:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the local score distribution.

SUMMARY:

ID	Score	Query	Length	DB ID	Description
1	84	81.6	289	13	Q9DC08
2	77	74.8	281	13	Q9DC09
3	66	64.1	285	6	Q9GM00
4	66	64.1	287	14	Q9DB04
5	66	64.1	287	13	Q9DB06
6	65	63.1	285	13	Q9DC10
7	45	41.7	634	2	G55412
8	44.5	41.2	446	2	Q9P509
9	44	42.7	1567	11	Q35143
10	44	42.7	1827	5	Q9DB05
11	44	42.7	1831	5	Q9M410
12	44	41.7	1831	5	Q9DB06
13	43	41.7	275	4	Q9NY05
14	43	41.7	459	5	Q26001
15	43	41.7	794	4	Q9H940
16	43	41.7	1135	13	Q9Y103
17	43	41.7	1211	4	Q94806
18	43	41.7	1259	5	Q44911
19	42.5	41.3	482	14	Q91457

20	42.5	41.3	521	13	Q91458
21	42	40.6	366	5	Q19278
22	42	40.6	539	14	Q55113
23	42	40.6	462	2	Q9RS07
24	42	40.6	584	5	Q9VLE7
25	42	40.6	891	4	Q9DB06
26	42	40.4	891	11	Q9AY76
27	42	40.4	1321	4	Q75129
28	42	40.4	2356	5	Q9X708
29	42	40.8	4545	2	Q9X462
30	42	40.8	4598	2	Q9X812
31	41.5	40.3	214	3	Q9P016
32	41.5	40.3	247	5	Q20018
33	41	39.8	124	5	Q9H006
34	41	39.8	205	4	Q15018
35	41	39.8	216	2	Q9F3X0
36	41	39.8	246	1	Q27417
37	41	39.8	269	2	Q9R029
38	41	39.3	271	3	Q9V118
39	41	39.3	238	2	Q9H026
40	41	39.3	421	11	Q62715
41	41	39.8	429	3	Q74862
42	41	39.8	445	3	Q94214
43	41	39.8	445	3	Q94215
44	41	39.8	445	3	Q900W5
45	41	39.8	803	3	Q74102

ALL SUMMARY

RESULT	1
Q9DC08	PHILIPINARIY
ID	Q9DC08
AC	Q9DC08
DE	01-MAR-2001 (TRENDEL 16, Creole)
DT	01-MAR-2001 (TRENDEL 16, last annotation update)
DR	01-MAR-2001 (TRENDEL 16, last annotation update)
DE	STEROIDOGENIC ACUTE REGULATORY PROTEIN (SRADMENT)
GN	SRAR
OS	Xenopus laevis (African clawed frog)
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Amphibia
OC	Amphibia; Batrachia; Anura; Mesobatrachia; Pipiloidea; Pipilidae
OC	Xenopodidae; Xenopus
OX	NCBI_TaxID:8455
RN	[1]
RP	SEQUENCE FROM N.A.
RC	TISSUE:OVARY
RX	PubMed-11064198
RA	Bauer M.P., Bricham J.T., Langston J.M., Polansky A.L., 2001, J. Biol. Chem. 276:11064-11068
RT	Conservation of steroidogenic acute regulatory (SRAR) protein
RL	Str. Mol. Cell. Biochem. 166:119-120 (2000)
DR	EMBL: AF220477; NCBI:295515
FT	NON_CODING
FT	NON_CODING
SO	SEQUENCE
Query Match	81.6%
Best Local Similarity	78.9%
Matches	15
Q9	1 GSTCVALAMATHHEMPED 19
DB	198 GSTCVALAMATHHEMPED 216
RESULT	2
Q9DC09	PHILIPINARIY
ID	Q9DC09
AC	Q9DC09
DE	01-MAR-2001 (TRENDEL 16, Creole)

FA van den Bosch C, Malavielle G, Jilka R, et al.: "CDNA DSC4 expressed by osteoclasts is an osteolytic stimulant." Submitted (MAE 2000) to the ENIGM Web site (<http://www.enigm.org>).
GC - 1. SIMILIARITY REGIONS TO THE NUCLEAR PORE PROTEIN-1 (NUP1)
DE EMBL: AF12768; AAF6515.1
DR InterPro: IPRO00952
DR InterPro: IPRO00922
DR Pfam: PF00936, 2f_02H2, 9.
DE PRINTS: PR00048; ZINCINGER
DE ProDom: PD00045, 2
DR PROSITE: PS00092; ZING_FINGER_ZNF2
KW DNA-binding; Metal-binding; Nuclear protein; Zinc finger domain
SO SPOUNCE: ZFY AA: A0781 MW: 52407.71 GRAVITY: 0.064

Query Match	41.78%	Score 4.7	149.42	Length 275
Post Local Similarity	47.19%	Percent M	45	
Matches	8	Conservative	2	Mismatch 7
QY	1	GSTCVLAAMTHFGEMD	17	
	11:11	11:11		
Db	144	GSSCLAHRIKTHFGEMD	160	

[illegible]

	41.78%	St. C.	6.9	1	1st	74%
Direct Match						
Bet. Local Similitude	100.0%	Nat. C.	6.7			
Matches	8	Match Score	3	4	Indels	67
CY	3	TOTAL MATCHES	18			
	3	1	1	1		
DB	95	SIMILARITY TYPE	110			

Search completed. A list of results is shown below.
Help: F1000: 1000 Search

01 NOV-1996 (TREMUREL, 01, Last sequence update)
 01 OCT-2000 (TREMUREL, 15, Last sequence update)
 DE ENO-1.4-HEXA-TRIMANASE (P04214) (Eno 1.4) (Nucleotide ANASE)
 05 Bacteria: sp.
 06 Bacteria: Firmicutes: Bacillus/Jordanella group
 07 Bacillus/Jordanella group (P04214)
 08 NCBI_TaxID: 1409;
 09 NCBI_TaxID: 1409;
 10 NCBI_TaxID: 1409;
 11 NCBI_TaxID: 1409;
 12 NCBI_TaxID: 1409;
 13 NCBI_TaxID: 1409;
 14 NCBI_TaxID: 1409;
 15 NCBI_TaxID: 1409;
 16 NCBI_TaxID: 1409;
 17 NCBI_TaxID: 1409;
 18 NCBI_TaxID: 1409;
 19 NCBI_TaxID: 1409;
 20 NCBI_TaxID: 1409;
 21 NCBI_TaxID: 1409;
 22 NCBI_TaxID: 1409;
 23 NCBI_TaxID: 1409;
 24 NCBI_TaxID: 1409;
 25 NCBI_TaxID: 1409;
 26 NCBI_TaxID: 1409;
 27 NCBI_TaxID: 1409;
 28 NCBI_TaxID: 1409;
 29 NCBI_TaxID: 1409;
 30 NCBI_TaxID: 1409;
 31 NCBI_TaxID: 1409;
 32 NCBI_TaxID: 1409;
 33 NCBI_TaxID: 1409;
 34 NCBI_TaxID: 1409;
 35 NCBI_TaxID: 1409;
 36 NCBI_TaxID: 1409;
 37 NCBI_TaxID: 1409;
 38 NCBI_TaxID: 1409;
 39 NCBI_TaxID: 1409;
 40 NCBI_TaxID: 1409;
 41 NCBI_TaxID: 1409;
 42 NCBI_TaxID: 1409;
 43 NCBI_TaxID: 1409;
 44 NCBI_TaxID: 1409;
 45 NCBI_TaxID: 1409;
 46 NCBI_TaxID: 1409;
 47 NCBI_TaxID: 1409;
 48 NCBI_TaxID: 1409;
 49 NCBI_TaxID: 1409;
 50 NCBI_TaxID: 1409;
 51 NCBI_TaxID: 1409;
 52 NCBI_TaxID: 1409;
 53 NCBI_TaxID: 1409;
 54 NCBI_TaxID: 1409;
 55 NCBI_TaxID: 1409;
 56 NCBI_TaxID: 1409;
 57 NCBI_TaxID: 1409;
 58 NCBI_TaxID: 1409;
 59 NCBI_TaxID: 1409;
 60 NCBI_TaxID: 1409;
 61 NCBI_TaxID: 1409;
 62 NCBI_TaxID: 1409;
 63 NCBI_TaxID: 1409;
 64 NCBI_TaxID: 1409;
 65 NCBI_TaxID: 1409;
 66 NCBI_TaxID: 1409;
 67 NCBI_TaxID: 1409;
 68 NCBI_TaxID: 1409;
 69 NCBI_TaxID: 1409;
 70 NCBI_TaxID: 1409;
 71 NCBI_TaxID: 1409;
 72 NCBI_TaxID: 1409;
 73 NCBI_TaxID: 1409;
 74 NCBI_TaxID: 1409;
 75 NCBI_TaxID: 1409;
 76 NCBI_TaxID: 1409;
 77 NCBI_TaxID: 1409;
 78 NCBI_TaxID: 1409;
 79 NCBI_TaxID: 1409;
 80 NCBI_TaxID: 1409;
 81 NCBI_TaxID: 1409;
 82 NCBI_TaxID: 1409;
 83 NCBI_TaxID: 1409;
 84 NCBI_TaxID: 1409;
 85 NCBI_TaxID: 1409;
 86 NCBI_TaxID: 1409;
 87 NCBI_TaxID: 1409;
 88 NCBI_TaxID: 1409;
 89 NCBI_TaxID: 1409;
 90 NCBI_TaxID: 1409;
 91 NCBI_TaxID: 1409;
 92 NCBI_TaxID: 1409;
 93 NCBI_TaxID: 1409;
 94 NCBI_TaxID: 1409;
 95 NCBI_TaxID: 1409;
 96 NCBI_TaxID: 1409;
 97 NCBI_TaxID: 1409;
 98 NCBI_TaxID: 1409;
 99 NCBI_TaxID: 1409;
 100 NCBI_TaxID: 1409;

01 NOV-1996 (TREMUREL, 01, Last sequence update)
 01 OCT-2000 (TREMUREL, 15, Last sequence update)
 DE ENO-1.4-HEXA-TRIMANASE (P04214) (Eno 1.4) (Nucleotide ANASE)
 05 Bacteria: sp.
 06 Bacteria: Firmicutes: Bacillus/Jordanella group
 07 Bacillus/Jordanella group (P04214)
 08 NCBI_TaxID: 1409;
 09 NCBI_TaxID: 1409;
 10 NCBI_TaxID: 1409;
 11 NCBI_TaxID: 1409;
 12 NCBI_TaxID: 1409;
 13 NCBI_TaxID: 1409;
 14 NCBI_TaxID: 1409;
 15 NCBI_TaxID: 1409;
 16 NCBI_TaxID: 1409;
 17 NCBI_TaxID: 1409;
 18 NCBI_TaxID: 1409;
 19 NCBI_TaxID: 1409;
 20 NCBI_TaxID: 1409;
 21 NCBI_TaxID: 1409;
 22 NCBI_TaxID: 1409;
 23 NCBI_TaxID: 1409;
 24 NCBI_TaxID: 1409;
 25 NCBI_TaxID: 1409;
 26 NCBI_TaxID: 1409;
 27 NCBI_TaxID: 1409;
 28 NCBI_TaxID: 1409;
 29 NCBI_TaxID: 1409;
 30 NCBI_TaxID: 1409;
 31 NCBI_TaxID: 1409;
 32 NCBI_TaxID: 1409;
 33 NCBI_TaxID: 1409;
 34 NCBI_TaxID: 1409;
 35 NCBI_TaxID: 1409;
 36 NCBI_TaxID: 1409;
 37 NCBI_TaxID: 1409;
 38 NCBI_TaxID: 1409;
 39 NCBI_TaxID: 1409;
 40 NCBI_TaxID: 1409;
 41 NCBI_TaxID: 1409;
 42 NCBI_TaxID: 1409;
 43 NCBI_TaxID: 1409;
 44 NCBI_TaxID: 1409;
 45 NCBI_TaxID: 1409;
 46 NCBI_TaxID: 1409;
 47 NCBI_TaxID: 1409;
 48 NCBI_TaxID: 1409;
 49 NCBI_TaxID: 1409;
 50 NCBI_TaxID: 1409;
 51 NCBI_TaxID: 1409;
 52 NCBI_TaxID: 1409;
 53 NCBI_TaxID: 1409;
 54 NCBI_TaxID: 1409;
 55 NCBI_TaxID: 1409;
 56 NCBI_TaxID: 1409;
 57 NCBI_TaxID: 1409;
 58 NCBI_TaxID: 1409;
 59 NCBI_TaxID: 1409;
 60 NCBI_TaxID: 1409;
 61 NCBI_TaxID: 1409;
 62 NCBI_TaxID: 1409;
 63 NCBI_TaxID: 1409;
 64 NCBI_TaxID: 1409;
 65 NCBI_TaxID: 1409;
 66 NCBI_TaxID: 1409;
 67 NCBI_TaxID: 1409;
 68 NCBI_TaxID: 1409;
 69 NCBI_TaxID: 1409;
 70 NCBI_TaxID: 1409;
 71 NCBI_TaxID: 1409;
 72 NCBI_TaxID: 1409;
 73 NCBI_TaxID: 1409;
 74 NCBI_TaxID: 1409;
 75 NCBI_TaxID: 1409;
 76 NCBI_TaxID: 1409;
 77 NCBI_TaxID: 1409;
 78 NCBI_TaxID: 1409;
 79 NCBI_TaxID: 1409;
 80 NCBI_TaxID: 1409;
 81 NCBI_TaxID: 1409;
 82 NCBI_TaxID: 1409;
 83 NCBI_TaxID: 1409;
 84 NCBI_TaxID: 1409;
 85 NCBI_TaxID: 1409;
 86 NCBI_TaxID: 1409;
 87 NCBI_TaxID: 1409;
 88 NCBI_TaxID: 1409;
 89 NCBI_TaxID: 1409;
 90 NCBI_TaxID: 1409;
 91 NCBI_TaxID: 1409;
 92 NCBI_TaxID: 1409;
 93 NCBI_TaxID: 1409;
 94 NCBI_TaxID: 1409;
 95 NCBI_TaxID: 1409;
 96 NCBI_TaxID: 1409;
 97 NCBI_TaxID: 1409;
 98 NCBI_TaxID: 1409;
 99 NCBI_TaxID: 1409;
 100 NCBI_TaxID: 1409;

PL Mol. Microbiol. 21:77-96(1996).
 DR EMBL: AL450165; CAC16436.1; ...
 KM Super Transpos.
 SO SEQUENCE 331 AA: 36866 MW: 40541.48125968 CR664.

Query Match 60.6% Score 49.0 DB: Length 695
 Best Local Similarity 63.6% Prod. No. 275
 Matches 7: Conservative 2: Mismatches 2: Indels 0: Gaps 0:

UY 2 LG11NDEGK 12
 DB 295 LG11NDEGK 295

RESULT 14
 U31773 PRELIMINARY: PRT: 97 AA.
 AC U31773;
 DT 01-NOV-1996 (TRENCH, J., created)
 DT 01-MAR-2001 (TRENCH, J., last version update)
 DT 01-MAR-2001 (TRENCH, J., last version update)
 NA08 DEHYDROGENASE SUBUNIT (FRAMING)
 NAME
 OS Atropa belladonna (belladonna).
 OC Chloroplast.
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Magnoliophyta; Eudicotyledones; Core eudicotyledons; Asteridales; Gentianales;
 OC Solanaceae; Solanaceae; Atropa.
 OX NCBI_TaxID=33133;
 RN [1]
 RP SEQUENCE OF 1-430 FROM N.A.
 RA Olmstead R.G., Bremer B., Scott R.M., Palmer J.D.
 KT "A parsimony analysis of the Asteridae sensu lato based on 18S
 RT rDNA sequences."
 RL Ann. Mo. Bot. Gard. 83:700-722(1996)
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Olmstead R.G., Bremer B., Scott R.M., Palmer J.D.
 KT "Combining data in phylogenetic systematics: an empirical approach
 RT using three molecular data sets in the Solanaceae."
 RL Syst. Biol. 43:457-481(1994).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Olmstead R.G.
 RL Submitted (Apr-1994) to the EMBL/GenBank/ DDBJ databases.
 DR EMBL: U08915; AAA18597.2; ...
 DR InterPro: IPR001516;
 DR InterPro: IPR001750;
 DR InterPro: IPR002128;
 DR Pfam: PF00361; oxidored_q1_1;
 Pfam: PF00662; oxidored_q1_N; 1;
 Pfam: PF01010; oxidored_q1_C; 1;
 KW Chloroplast.
 FT NON_TER 1
 FT NON_TER 695
 SO SEQUENCE 695 AA: 78723 MW: 6296251709527 CR664.

Query Match 60.6% Score 49.0 DB: Length 695
 Best Local Similarity 63.6% Prod. No. 275
 Matches 7: Conservative 2: Mismatches 2: Indels 0: Gaps 0:

UY 1 ALG11NDEGK 11
 DB 550 ALG11NDEGK 550

RESULT 15
 U00851 PRELIMINARY: PRT: 119 AA.
 ID U00851;
 AC U00851;
 DT 01-JUL-1997 (TRENCH, J., created).

DT 01-JUL-1997 (TRENCH, J., last version update)
 DT 01-MAR-2001 (TRENCH, J., last version update)
 DE UNCONVENTIONAL MYOSIN IB.
 OS Eukaryota; Eukaryota; Eukaryota;
 OX NCBI_TaxID=5759;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Vargha M., Varga B., Sansonetti P., ...
 RT "Molecular characterization of myosin IB from the ...
 RT Eukaryota histology, a human paralogous."
 RL Mol. Biochem. Parasitol. 86:141-143(1997)
 DR EMBL: U08955; AA47535.1;
 DR HSP: P08799; IBM.
 DR InterPro: IPR01452;
 DR InterPro: IPR01609;
 DR Pfam: PF00018; SH3_1;
 DR Pfam: PF00064; myosin_head_1;
 DR PRINTS: PR00159; MYOSINHEAVY;
 DR PRINTS: PR00452; SH3B6A1N;
 DR TrEMBL: P000455; ...
 DR PRSITE: PS00024; SH3_1;
 DR SMART: SM00427; SH3_1;
 SO SEQUENCE 1049 AA: 119551 MW: 119551 CR664.

Query Match 60.6% Score 49.0 DB: Length 1049
 Best Local Similarity 77.8% Prod. No. 992
 Matches 7: Conservative 0: Mismatches 2: Indels 0: Gaps 0:

UY 3 G11NDEGK 11
 DB 1632 G11NDEGK 1632

Search completed: August 22, 2001, 14: 25.4
 Job time: 198 sec

Wed Aug 22 15:43:01 2001

us-08-659-254-4.rspt

Page 6

Query Match: 100.0% Score: 1.4, 28.20, 28.20, 28.20
 Best Local Similarity: 100.0% Prod. No. 28-082
 Matches: 19; Conserved: 0; Misses: 0; Gaps: 0

QY 1 GSTCVMAMHHEPMPQ 19
 |||
 DB 194 gstrclapmarchmpq 211

RESULT 4
 AAV72831
 ID AAV72831 standard; Protein: 284 AA

AC AAV72831:
 DE 41-MAY-2001 (first entry)
 DE Mouse steroidogenic acute regulatory (STAR) protein
 KW Mouse; steroidogenic acute regulatory protein; STAR;
 KW gene therapy; steroid hormone-dependent; lipid; lipid
 KW lipid congenital adrenal hyperplasia; sexual maturation;
 KW infertility; androgen-responsive tumor; precocious puberty;
 KW hypogonadotropic hypogonadism; Klinefelter syndrome;
 KW adrenal-hypoplasia congenita; cytosol

OS Mus sp.
 PH Key: Location/Qualifiers
 FT peptide
 FT /label Signal_peptide
 FT /note "Site for mitochondrial processing;
 FT matrix-processing protease and mitochondrial
 FT intermediate processing peptide"
 FT 48..284
 FT /label Mature_steroidogenic_acute_regulatory_protein
 FT 49..50
 FT /note "Site for mitochondrial processing;
 FT matrix-processing protease and mitochondrial
 FT intermediate processing peptide"
 FT 59..60
 FT /note "PKA phosphorylation site"
 FT 58..69
 FT /note "CK phosphorylation site"
 FT 85..96
 FT /label Tyrosine_Tyr_#25
 FT 88..98
 FT /note "This sequence is used to raise antibodies
 FT against STAR protein"
 FT 193..211
 FT /label Tyrosine_Tyrosine_#45
 FT 195
 FT /note "PKA phosphorylation site"
 FT 232..240
 FT /label Tyrosine_Tyrosine_#24
 FT 233..234
 FT /note "P340C2 kinase (CK) phosphorylation site"
 FT 238
 FT /note "PKC phosphorylation site"

FT Modified-site
 FT 195
 FT /note "PKA phosphorylation site"
 FT 232..240
 FT /label Tyrosine_Tyrosine_#24
 FT 233..234
 FT /note "P340C2 kinase (CK) phosphorylation site"
 FT 238
 FT /note "PKC phosphorylation site"

PN US6194555-B1
 XX 27-FEB-2001
 XX
 XX 07-JUN-1996; 9608-0659254
 PE
 XX 04-MAY-1995; 9505-0589660
 XX
 XX (UNITE-) UNIV TEXAS TECH HEALTH SCI CENT
 PA
 XX Stocco DM, Clark MJ

XX
 DE W01: 2801: 237: 4722
 DE N (SDS: AAM02902; AAM02902)
 XX
 DE Novel nucleic acid encoding steroidogenic acute regulatory protein
 PT useful for treating steroid hormone-dependent disorders
 PT
 XX
 DE Example 2: Fig 2: 41pp: English

XX
 DE The invention relates to steroidogenic acute regulatory protein
 DE (STAR) and nucleic acid molecules encoding them. STAR proteins
 DE are used for regulating steroidogenesis. More particularly these
 DE proteins are involved in regulating cholesterol transport into
 DE the mitochondria of a cell. The nucleic acid molecules of the
 DE invention are useful in gene therapy for the treatment of steroid
 DE hormone dependent disorders, particularly lipid congenital
 DE adrenal hyperplasia (LHAI), infertility, sexual maturation,
 DE androgen-responsive tumors, precocious puberty, Klinefelter
 DE syndrome, adrenal hypoplasia congenita and hypogonadotropic
 DE hypogonadism. They are also useful for recombinant preparation
 DE of the steroidogenic acute regulatory protein.
 DE The present sequence is mouse steroidogenic acute regulatory
 DE protein (STAR).

SO Sequence: 284 AA

Query Match: 100.0% Score: 1.4, 28.20, 28.20, 28.20
 Best Local Similarity: 100.0% Prod. No. 28-082
 Matches: 19; Conserved: 0; Misses: 0; Gaps: 0

QY 1 GSTCVMAMHHEPMPQ 19
 |||
 DB 194 gstrclapmarchmpq 211

RESULT 5
 AAV72838
 ID AAV72838 standard; Protein: 284 AA

AC AAV72838:
 DE 41-MAY-2001 (first entry)
 DE Human steroidogenic acute regulatory (STAR) protein
 KW Human; steroidogenic acute regulatory protein; STAR;
 KW gene therapy; steroid hormone-dependent; lipid; lipid
 KW lipid congenital adrenal hyperplasia; sexual maturation;
 KW infertility; androgen-responsive tumor; precocious puberty;
 KW hypogonadotropic hypogonadism; Klinefelter syndrome;
 KW adrenal hyperplasia congenita; cytosol

OS Homo sapiens
 PH Key: Location/Qualifiers
 FT peptide
 FT /note "Encoded by cDNA. This protein corresponds
 FT to the translation except for the sequence shown
 FT in (AAM02902)"
 FT 59..60
 FT /note "PKA phosphorylation site"
 FT 58..69
 FT /note "CK phosphorylation site"
 FT 85..96
 FT /note "PKA phosphorylation site"
 FT 88..98
 FT /note "This sequence is used to raise antibodies
 FT against STAR protein"
 FT 193..211
 FT /label Tyrosine_Tyrosine_#45
 FT 195
 FT /note "PKA phosphorylation site"
 FT 232..240
 FT /label Tyrosine_Tyrosine_#24
 FT 233..234
 FT /note "P340C2 kinase (CK) phosphorylation site"
 FT 238
 FT /note "PKC phosphorylation site"

FT Modified-site
 FT 195
 FT /note "PKA phosphorylation site"
 FT 232..240
 FT /label Tyrosine_Tyrosine_#24
 FT 233..234
 FT /note "P340C2 kinase (CK) phosphorylation site"
 FT 238
 FT /note "PKC phosphorylation site"

PN US6194555-B1
 XX 27-FEB-2001
 XX
 XX 07-JUN-1996; 9608-0659254
 PE
 XX 04-MAY-1995; 9505-0589660
 XX
 XX (UNITE-) UNIV TEXAS TECH HEALTH SCI CENT
 PA
 XX Stocco DM, Clark MJ

Query Match 80.68: Score 84.16 Length 285
 Best Local Similarity 84.28: Pctid: No: 1.36 (2)
 Matches 16: Conservative 0: Mismatches 4: Indels 0: Gaps 1

QY 1 GSPCVIACMAIHPHMPQ 19
 (|||||) 1 (|||||)
 Db 194 qstcvlaamdtdtqmpq 212

RESULT 12
 AAM13235
 ID AAM13235 standard: Protein: 285 AA

XX AAM13235

XX 21-MAY-1997 (first entry)

XX Human steroidogenesis acute regulatory protein mutant (HAP498)

XX Human steroidogenesis acute regulatory protein (HAP) and HAP498

XX mutation: detection: prenatal: genetic: congenital: adrenal: hypoplasia:

XX replacement therapy: hypercholesterolemia: mutant

XX Homo sapiens

XX Key Location/Qualifiers

XX Misc-difference 169 /note="wild type 3-4 substituted with 199"

XX W09629438-A1

XX 26-SEP-1996

XX 22-MAR-1996: 96WD-0803896

XX 23-MAR-1995: 95DS-0410540

XX (RRCG) UNIV CALIFORNIA

XX (UTPE) UNIV PENNSYLVANIA

XX Lin D, Miller WL, Strauss JF

XX WPI: 1996-44130/44

XX N-PSDB: AAT62020

XX Isolated human steroidogenesis acute regulatory protein gene used

XX for detection of mutation(s) of this gene that cause congenital

XX Lipoid adrenal hyperplasia

XX Claim 13: Page: 89pp: English

XX The present sequence is the human steroidogenesis acute regulatory

XX protein (HAP), congenital lipoid adrenal hyperplasia (GLAH)

XX associated mutant, Q14595ys. According to the HAP gene, each a

XX mutation is useful in the detection (e.g., prenatal) of GLAH

XX associated genetic defects, or its transmission to children. HAP

XX can be treated by protein or gene replacement therapy, which can

XX also be used to prevent or treat hypercholesterolemia.

XX Sequence 285 AA

RESULT 13

AAK98454

15 AAK98454 standard: Protein: 413 AA

XX AAK98454

XX 15-SEP-1996 (first entry)

XX Oligodendrocyte myelin glycoprotein

XX Oligodendrocyte myelin glycoprotein (MSP) (P-18 protein)

XX central nervous system (CNS) myelin and oligodendrocytes

XX diagnosis

XX Homo sapiens

XX Key Location/Qualifiers

XX Peptide

XX Misc-difference 14

XX Domain

XX Domain

XX Domain

XX Domain

XX Domain

XX Domain

XX Domain

XX Domain

XX Domain

XX Domain

XX Domain

XX Domain

XX Domain

XX Domain

XX Domain

XX Domain

XX Domain

XX Domain

XX Domain

XX Domain

XX Domain

XX Domain

XX Domain

XX Domain

Linkage analysis, and for locating gene regions associated with genetic disease, to control gene expression. The cDNAs, transcripts, and expression products are useful as: (1) genome markers for determining the location of genes with the genome and articles expressed, during the development of cultured fetal mesenchymal cells. The cDNAs are also useful in detecting the presence of mutations in genes leading to diseases affecting bone growth, by comparing the sequences with those found in similar chromosomal locations in mammals, especially humans afflicted with diseases affecting bone growth, in human fibroblasting and bone marrow, the polypeptides encoded by the mesenchymal stem cell cDNAs or peptide fragments, derivatives, analogs or cells expressing them are useful as immunogens for the production of antibodies.

Sequence: 275 AA:

Query Match: 41.7% Score 45 (P 21) Length 275
Best Local Similarity: 47.1% Prod. No. 512
Matches: 8: Conservative 2: Mismatch 7: Indels 1: Gaps

On: 1 GSTVLAAMAHFGMP 17
1111 1111
144 uucclarrhrrhrrp 160

Search completed: August 22, 2001, 14:54:11
Job time: 304 sec



RESULT

US 08 659 254 5

Sequence No. Application 15/0005254

Patent No. 61490

GENERAL INFORMATION

APPLICANT: SHIMADZU, KIMURA

APPLICANT: SHIMADZU, KIMURA

TITLE OF INVENTION: METHOD FOR

NUMBER OF SHEETS: 10

ADDRESS: 1-1-1, SHIMADZU, KIMURA

STREET: 1-1-1, SHIMADZU, KIMURA

CITY: AUSTIN

STATE: TX

COUNTRY: U.S.A.

ZIP: 78701

COMPUTER RESEARCH

MEDIUM TYPE: 1000000000

COMPUTER: 1000000000

OPERATING SYSTEM: 1000000000

SOFTWARE: 1000000000

CURRENT APPLICATION NO.

APPLICATION NUMBER 15/0005254

FILING DATE 10/1/00

CLASSIFICATION 50

PRIORITY APPLICATION NO.

APPLICATION NUMBER 15/0005254

FILING DATE 10/1/00

CLASSIFICATION 50

PRIORITY APPLICATION NO.

APPLICATION NUMBER 15/0005254

FILING DATE 10/1/00

CLASSIFICATION 50

PRIORITY APPLICATION NO.

APPLICATION NUMBER 15/0005254

FILING DATE 10/1/00

CLASSIFICATION 50

PRIORITY APPLICATION NO.

APPLICATION NUMBER 15/0005254

FILING DATE 10/1/00

CLASSIFICATION 50

PRIORITY APPLICATION NO.

APPLICATION NUMBER 15/0005254

FILING DATE 10/1/00

CLASSIFICATION 50

PRIORITY APPLICATION NO.

APPLICATION NUMBER 15/0005254

FILING DATE 10/1/00

CLASSIFICATION 50

PRIORITY APPLICATION NO.

APPLICATION NUMBER 15/0005254

FILING DATE 10/1/00

CLASSIFICATION 50

PRIORITY APPLICATION NO.

APPLICATION NUMBER 15/0005254

FILING DATE 10/1/00

CLASSIFICATION 50

PRIORITY APPLICATION NO.

APPLICATION NUMBER 15/0005254

FILING DATE 10/1/00

CLASSIFICATION 50

PRIORITY APPLICATION NO.

APPLICATION NUMBER 15/0005254

FILING DATE 10/1/00

CLASSIFICATION 50

PRIORITY APPLICATION NO.

APPLICATION NUMBER 15/0005254

FILING DATE 10/1/00

SEQUENCE CHARACTERISTICS:
 LENGTH: 284 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-659-254-2

Query Match: 100.0% Score 114.0E+2 Length 284
 Best Local Similarity: 100.0% Pident No: 1.4E+09
 Matches: 19; Conservative 0; Mismatch 0; Indels 0; Gaps 0

QY 1 GSTCVLAGMAHREMPD 19
 DB 194 GSTCVLAGMAHREMPD 211

RESULT 5
 US-08-659-254-18
 Sequence 18; Application US-08659-074
 Patent No. 6194555

GENERAL INFORMATION:
 APPLICANT: Stecco, Douglas M.
 APPLICANT: Clark, Dr. Barbara J.
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR REGULATION
 NUMBER OF SEQUENCES: 19
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Akin, Gump, Strauss, Hoot & Fold, L.L.P.
 STREET: 1600 Frost Bank Plaza, 8100 Ross Avenue
 CITY: Austin
 STATE: TX
 COUNTRY: U.S.A.
 ZIP: 78701

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0; Version #1.00
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US-08/659,254
 FILING DATE: 07-JUN-1996
 CLASSIFICATION: 530
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US-08/538,460
 FILING DATE: 04-OCT-1995

ATTORNEY/AGENT INFORMATION:
 NAME: Magtilla, Denise L.
 REGISTRATION NUMBER: 34742
 REFERENCE/DOCKET NUMBER: 43375, 006
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 512/499-6200
 TELEFAX: 512/797-6290

INFORMATION FOR SEQ ID NO: 18:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 285 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 US-08-659-254-18

Query Match: 80.4% Score 89.0E+1 Length 285
 Best Local Similarity: 89.5% Pident No: 2.9E+07
 Matches: 17; Conservative 0; Mismatch 3; Indels 0; Gaps 0

QY 1 GSTCVLAGMAHREMPD 19
 DB 194 GSTCVLAGMAHREMPD 212

RESULT 6
 US-08-410-540-2

Sequence 2; Application US-08410540

Patent No. 5807678
 GENERAL INFORMATION:
 APPLICANT: Miller, Walter L.
 APPLICANT: Liu, Dong
 APPLICANT: Straus III, Jerome F.
 TITLE OF INVENTION: IDENTIFICATION OF GENE MUTAT
 NUMBER OF SEQUENCES: 40
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Volney Godward Castro Buddeson & Parnum
 STREET: 5 Palo Alto Square
 CITY: Palo Alto
 STATE: CA
 COUNTRY: US
 ZIP: 94301-2145

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0; Version #1.00
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US-08/410,540
 FILING DATE: 23-MAR-1995
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Nealey, Richard L.
 REGISTRATION NUMBER: 30,092
 REFERENCE/DOCKET NUMBER: 00A-247,001S

TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415 853 5070
 TELEFAX: 415 857 0663
 TELEX: 380816COOLEVPA
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 285 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-410-540-2

Query Match: 80.6% Score 89.0E+1 Length 285
 Best Local Similarity: 84.2% Pident No: 4.3E+09
 Matches: 16; Conservative 0; Mismatch 3; Indels 0; Gaps 0

QY 1 GSTCVLAGMAHREMPD 19
 DB 194 GSTCVLAGMAHREMPD 212

RESULT 7
 US-08-659-052-4

Sequence 4; Application US-08659052
 Patent No. 5849498
 GENERAL INFORMATION:
 APPLICANT: Bancman, Olga
 APPLICANT: Guellet, Karl J.
 APPLICANT: Shalt, Perry
 APPLICANT: Farley, Scott
 TITLE OF INVENTION: HUMAN 3 INTER-
 TITLE OF INVENTION: HYDROLASE
 NUMBER OF SEQUENCES: 4
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Inglethorne, Inc.
 STREET: 474 Porter Drive
 CITY: Palo Alto
 STATE: CA
 COUNTRY: USA
 ZIP: 94304

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM compatible

Query Match 38.8% Score 401 Len 11 Length 3997
 Best Local Similarity 53.8% Pred No 607
 Matches 77 Conservative 43 Mismatches 32 Indels 0 Gaps 0
 QY 8 TCIVLALATVGE 20
 11: 11 111

RESULT 10
 US-08-477-108A-6
 Sequence 6, Application US/08477108A
 Patent No. 5801001

GENERAL INFORMATION:
 APPLICANT: Sager, Ruth
 APPLICANT: Sager, Ruth
 APPLICANT: Sager, Ruth
 TITLE OF INVENTION: MASTIN, A NEWLY DISCOVERED WITH
 TITLE OF INVENTION: TUMOR SUPPRESSING ACTIVITY
 NUMBER OF SEQUENCES: 11
 CORRESPONDENCE ADDRESS:
 ADDRESS: Fish & Richardson P.C.
 STREET: 225 Franklin Street
 CITY: Boston
 STATE: Massachusetts
 COUNTRY: U.S.A.
 ZIP: 02110-2804

COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5" Diskette, 1.44 MB
 COMPUTER: IBM PS/2 Model 502 or 505
 OPERATING SYSTEM: MS-DOS (Version 5.0)
 SOFTWARE: WordPerfect (Version 5.1)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/477-1-6
 FILING DATE: June 7, 1995
 CLASSIFICATION: 536
 PRICE APPLICATION DATA:
 APPLICATION NUMBER: 08/121,711
 FILING DATE: 09/01/94
 APPLICATION NUMBER: 07/948,824
 FILING DATE: 09/01/92
 APPLICATION NUMBER: 07/844,276
 FILING DATE: 02/28/92
 APPLICATION NUMBER: 07/662,216
 FILING DATE: 02/28/91
 ATTORNEY/AGENT INFORMATION:
 NAME: Fraser, Janis K.
 REGISTRATION NUMBER: 34,819
 REFERENCE/DOCKET NUMBER: 06570/0-6
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 542-5070
 TELEFAX: (617) 542-8906
 TELEX: 200154

INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 390
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 US-08-477-108A-6

Query Match 38.8% Score 401 Len 11 Length 3997
 Best Local Similarity 53.8% Pred No 607
 Matches 77 Conservative 43 Mismatches 32 Indels 0 Gaps 0
 QY 8 TCIVLALATVGE 20
 11: 11 111

RESULT 11

US-08-477-112-6
 Sequence 6, Application US/08477112
 Patent No. 5905024

GENERAL INFORMATION:
 APPLICANT: Sager, Ruth
 APPLICANT: Sager, Ruth
 APPLICANT: Sager, Ruth
 TITLE OF INVENTION: MASTIN, A NEWLY DISCOVERED WITH
 TITLE OF INVENTION: TUMOR SUPPRESSING ACTIVITY
 NUMBER OF SEQUENCES: 8
 CORRESPONDENCE ADDRESS:
 ADDRESS: Fish & Richardson P.C.
 STREET: 225 Franklin Street
 CITY: Boston
 STATE: Massachusetts
 COUNTRY: U.S.A.
 ZIP: 02110-2804

COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5" Diskette, 1.44 MB
 COMPUTER: IBM PS/2 Model 502 or 505
 OPERATING SYSTEM: MS-DOS (Version 5.0)
 SOFTWARE: WordPerfect (Version 5.1)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/477-1-6
 FILING DATE: June 7, 1995
 CLASSIFICATION: 536
 PRICE APPLICATION DATA:
 APPLICATION NUMBER: 08/121,711
 FILING DATE: 09/01/94
 APPLICATION NUMBER: 07/948,824
 FILING DATE: 09/01/92
 APPLICATION NUMBER: 07/844,276
 FILING DATE: 02/28/92
 APPLICATION NUMBER: 07/662,216
 FILING DATE: 02/28/91
 ATTORNEY/AGENT INFORMATION:
 NAME: Fraser, Janis K.
 REGISTRATION NUMBER: 34,819
 REFERENCE/DOCKET NUMBER: 06570/0-6
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 542-5070
 TELEFAX: (617) 542-8906
 TELEX: 200154

INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 390
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 US-08-477-112-6

Query Match 38.8% Score 401 Len 11 Length 3997
 Best Local Similarity 53.8% Pred No 607
 Matches 77 Conservative 43 Mismatches 32 Indels 0 Gaps 0
 QY 8 TCIVLALATVGE 20
 11: 11 111

RESULT 12
 US-08-477-112-6
 Sequence 6, Application US/08477112
 Patent No. 5905024

GENERAL INFORMATION:
 APPLICANT: Sager, Ruth
 APPLICANT: Sager, Ruth
 APPLICANT: Sager, Ruth
 TITLE OF INVENTION: MASTIN, A NEWLY DISCOVERED WITH
 TITLE OF INVENTION: TUMOR SUPPRESSING ACTIVITY
 NUMBER OF SEQUENCES: 8
 CORRESPONDENCE ADDRESS:
 ADDRESS: Fish & Richardson P.C.
 STREET: 225 Franklin Street
 CITY: Boston
 STATE: Massachusetts
 COUNTRY: U.S.A.
 ZIP: 02110-2804

COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5" Diskette, 1.44 MB
 COMPUTER: IBM PS/2 Model 502 or 505
 OPERATING SYSTEM: MS-DOS (Version 5.0)
 SOFTWARE: WordPerfect (Version 5.1)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/477-1-6
 FILING DATE: June 7, 1995
 CLASSIFICATION: 536
 PRICE APPLICATION DATA:
 APPLICATION NUMBER: 08/121,711
 FILING DATE: 09/01/94
 APPLICATION NUMBER: 07/948,824
 FILING DATE: 09/01/92
 APPLICATION NUMBER: 07/844,276
 FILING DATE: 02/28/92
 APPLICATION NUMBER: 07/662,216
 FILING DATE: 02/28/91
 ATTORNEY/AGENT INFORMATION:
 NAME: Fraser, Janis K.
 REGISTRATION NUMBER: 34,819
 REFERENCE/DOCKET NUMBER: 06570/0-6
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 542-5070
 TELEFAX: (617) 542-8906
 TELEX: 200154

OY 3 TVIACATP02 15
 11: 11: 111
 DB 8 TVIACATP02 20

Search completed. August 22, 2001, 14:30:11
 Job time: 365 sec

RESULT 15
 US-08-677-049-12

Sequence 12, Application US/08677049

Patent No. 5858707

GENERAL INFORMATION:

APPLICANT: Guimaraes, M. Jorge

APPLICANT: Bazan, J. Fernando

APPLICANT: McClanahan, Terrell K.

APPLICANT: Zlotnik, Albert

TITLE OF INVENTION: PURIFIED MAMMALIAN NUCLEOPHASE PREPARATIONS

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:

ADDRESS: DNA Research Institute

STREET: 901 California Avenue

CITY: Palo Alto

STATE: California

COUNTRY: USA

ZIP: 94304-1104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.00

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/98/677,049

FILING DATE: 03-JUL-1996

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/000,788

FILING DATE: 03-JUL-1996

ATTORNEY/AGENT INFORMATION:

NAME: Ching, Edwin P.

REGISTRATION NUMBER: 34,090

REFERENCE/DOCKET NUMBER: DX0511

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-852-9196

TELEFAX: 415-496-1200

INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:

LENGTH: 580 amino acids

TYPE: amino acid

STRANDEDNESS: Single

TOPOLOGY: linear

MOLECULE TYPE: protein

FEATURE:

NAME/KEY: Region

LOCATION: 207..236

OTHER INFORMATION: /note "Discusses IM 4 of Figure

OTHER INFORMATION: 4"

NAME/KEY: Region

LOCATION: 437..499

OTHER INFORMATION: /note "Discusses IM 9 and IM 10

OTHER INFORMATION: of Figure 4"

US-08-677-049-12

Query Match 38.8% Score 49. Dk 27 Length 580

Host Local Similarity 63.6% Prog. N 78

Matches 7: Conservative 2: Mismatch 4: Indels 0: Gap 0

OY 1 GSTVACAT 11

1 11:11:11

DB 388 GITCLAGCT 398

CC THE FETAL OVARY

CC -1 SIMILARITY: BELONGS TO THE SIAI FAMILY

CC This SWISS-Prot entry is copyright © 1992-2001, produced through a collaboration

CC between the Swiss Institute of Bioinformatics and the EMBL outstation

CC the European Bioinformatics Institute. There are no restrictions on its

CC use by non-profit institutions, but as its content is in no way

CC modified and this statement is not removed, usage by and for commercial

CC entities requires a license agreement with the EMBL outstation or

CC or send an email to license@ebi.ac.uk

CC

CC EMBL: 054020; AAB04953.1

CC EMBL: 072195; AAB30555.1

CC InterPro: IPR000739; 1

CC InterPro: IPR002913; 1

CC Pfam: PF01852; START; 1

CC PRINTS: PR00978; STAPROPELIN

CC Lipid-binding; Lipid transport; Transmembrane steroid-binding

CC Mitochondrion; Transit peptide

CC IT IPANST 1 2

CC CHAIN 2 285

CC CONFLICT 188 188

CC SPOONCE 285 AA: 31833 MW: 67026.9 kDa

Query Match 81.8% Score 24.00 E: Length 285

Best Local Similarity 83.4% Prod No. 00000001

Matches 10: Conservative 1: Moderate 1: Distant 0: Gaps 0

DB 86 ALDILNPGMK 97

UY 1 ALDILNPGMK 12

1111111111

RESULT 8

DB3_SCHPO STANDARD: PRI: 15 AA

AC 140984:

DT 01-FEB-1995 (Rel. 31, Created)

DT 01-FEB-1995 (Rel. 31, Last sequence update)

DT 01-OCT-1996 (Rel. 34, Last annotation update)

DE 0810011N-CONJUGATING ENZYME E2-19 K16 (P06332.1)

DE 0810011N-PROTEIN LIGASE H995 (0810011N-MAKREIN PROTEIN H995)

DE H995 OR SPAC300D11.13

OS Schizosaccharomyces pombe (Fission yeast)

OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;

OC Schizosaccharomyces; Schizosaccharomyces pombe

OC Schizosaccharomycetes

OC NCBI_TaxID=4896;

OK 11

RM SEQUENCE FROM N.A.

AL-Khodadi F., Enoch T., Hartman L.M., Ditt A.M.

RT The Schizosaccharomyces pombe has been studied as a model

RT conjugating enzyme required for normal mitosis.

RL J. Cell Sci. 106:475-486(1995).

RL 12

RP SEQUENCE FROM N.A.

RC STRAIN=972;

RA Pearson D., Church G.M., Bartell P., Kalandian M.A., Walsh S.V.

KL Submitted (NOV-1995) to the EMBL outstation

CC -1 FUNCTION: CATALYZES THE CATALYTIC INHERITANCE OF THE

CC OTHER PROTEINS. PRODUCE THE CATALYTIC INHERITANCE OF THE

CC S-PHASE ARREST AND NORMAL MITOSIS. THIS MAY BE AS PART OF A

CC CHECKPOINT INDEPENDENT RECOVERY MECHANISM.

CC -1 CATALYTIC ACTIVITY: ATP + H₂O → ADP + H₂PO₄ + H₂O

CC -1 PATHWAY: SECOND STEP IN UBIQUITIN CONJUGATION.

CC -1 SUBCELLULAR LOCATION: NUCLEAR

CC -1 MISCELLANEOUS: A CYSTEINE RESIDUE IS REQUIRED FOR

CC UBIQUITIN-THIOLESTER FORMATION

CC -1 SIMILARITY: BELONGS TO THE PRG1011 N-NUCLEOTIDYL TRANSFERASE FAMILY

CC STRONGEST, TO YEAST UBC9.

CC This SWISS-Prot entry is copyright © 1992-2001, produced through a collaboration

CC between the Swiss Institute of Bioinformatics and the EMBL outstation

CC the European Bioinformatics Institute. There are no restrictions on its

CC use by non-profit institutions, but as its content is in no way

CC modified and this statement is not removed, usage by and for commercial

CC entities requires a license agreement with the EMBL outstation or

CC or send an email to license@ebi.ac.uk

CC

CC EMBL: X01846; AAA7408.1

CC EMBL: Z67961; AAA1899.1

CC HSSP: P50550; IAB5

CC InterPro: IPR000108; 1

CC Pfam: PF00179; UC cons. 1

CC PRINTS: PR00194; PR00194

CC PROSITE: PS00127; PR00127

CC UBIQUITIN CONJUGATING ENZYME E2-19 K16 (P06332.1)

CC Ubiquitin conjugation; Ubiquitin-DNA repair; Nuclear protein

CC Multimeric family

CC BINDING 93 93

CC SPOONCE 173 AA: 17389 MW: 46466.0 kDa

Query Match 71.2% Score 67.40 E: Length 173

Best Local Similarity 72.7% Prod No. 00000001

Matches 8: Conservative 1: Moderate 2: Distant 0: Gaps 0

DB 94 LSTINERMK 104

UY 2 LSTINERMK 12

1111111111

RESULT 9

DB3_SCHPO STANDARD: PRI: 15 AA

AC 140984:

DT 01-JAN-1988 (Rel. 06, Created)

DT 01-JAN-1988 (Rel. 06, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE ENDOGLUCANASE PRECURSOR (EC 3.2.1.13) (Gene 1.4-DE-A-GLUCANASE)

DE (ALKALINE CELLULASE)

OS Bacillus sp. (strain 1139)

OC Bacteria; Firmicutes; Bacillus/Clustidium group

OC Bacillus/Clustidium group; Bacillus

OC NCBI_TaxID=1411;

OK 11

RM SEQUENCE FROM N.A.

MEHLIN 6795417; Pubmed 3096997

FA Fukumori F., Kudo T., Nishihashi Y., Hattosaka K.

RT Molecular cloning and nucleotide sequence of the alkaline cellulase

RT gene from the alkalophilic bacterium strain 1139.

RL J. Gen. Microbiol. 132:2429-2435(1999).

CC -1 CATALYTIC ACTIVITY: ENDOGLUCANASE (EC 3.2.1.13) (Gene 1.4-DE-A-GLUCANASE)

CC LINKAGE: IN CELLULOSE

CC -1 KINETICS: K_m = 1.7 x 10⁻³ M; V_{max} = 1.1 x 10⁻³ U/mg

CC ONE ALKALINE CELLULASE (THE 1139 K16) THE STRAIN IS NOT A

CC CELLULOSE (THE 1139 K16) THE STRAIN IS NOT A

CC HYDROLYSE NATIVE CELLULOSE

CC -1 SIMILARITY: BELONGS TO THE PRG1011 N-NUCLEOTIDYL TRANSFERASE FAMILY

CC STRONGEST, TO YEAST UBC9

CC

CC This SWISS-Prot entry is copyright © 1992-2001, produced through a collaboration

CC between the Swiss Institute of Bioinformatics and the EMBL outstation

CC the European Bioinformatics Institute. There are no restrictions on its

CC use by non-profit institutions, but as its content is in no way

CC modified and this statement is not removed, usage by and for commercial

CC entities requires a license agreement with the EMBL outstation or

CC or send an email to license@ebi.ac.uk

CC

CC EMBL: M15743; AAA22405.1

CC EMBL: D60964; AAA03845.1

CC PIR: A29003; A29003

CC InterPro: IPR001547; 1

CC Pfam: PF001547; Cellulase 1

CC The European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is not
 CC modified and this statement is not removed, altered or used by any other
 CC entity; requires a license agreement for commercial use.
 CC or send an email to license@ebi.ac.uk
 CC
 DR EMBL: D14003; AAA97227.1; ALT_INTL
 DR EMBL: AF00503; AAC77287.1; ALT_INTL
 DR F03000; EG12570; PTA
 DR InterPro: IPR002745
 DR Pfam: PF01853; D0F603.1
 DR Transferrase; MAD
 SQ SEQUENCE 184 AA: 20529 MW: 206348.772E+04 180664

Query Match: 57.6%; Score 381; ID 1; Length 184
 Best Local Similarity 54.5%; Prod. No. 74
 Matches 6; Conservative 4; Mismatch 1; Indels 0; Gaps 0

QY 1 ALG1NPGCW 11
 I:11:1111
 DP 26 ALG1VLRKRW 46

RESULT 12
 BGL1_FAC50 STANDARD: PRI: 100 AA
 ID BGL1_FAC50 STANDARD: PRI: 100 AA
 AC P40740; 032287;
 DT 01-FEB-1995 (rel. 3), Created
 DI 30 MAY 2000 (rel. 49, Last sequence update)
 DT 30 MAY 2000 (rel. 49, Last annotation update)
 DE BETA-GLUCOSIDASE (EC 3.2.1.21) (C) N1 (5 Ash) (CELLULOSE) (BETA)
 DE GLUCOSIDIC GLUCOHYDROLASE (AMYLASE) (BETA)
 GN BGL OR N1ZD
 OS Bacillus subtilis
 OC Bacillus; Firmicutes; Bacillus/Clostridia group
 OC Bacillus/Staphylococcus group; Bacillus
 OX NCBI_TaxID:1423
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN:168 / MAPPING
 RX MEDLINE:95189730; PubMed:7883710;
 RA Le Cou D.G., Linner G., Krueger S., Shimizu M., Stracke J.
 RT "New beta-glucoside (bgl) genes in Bacillus subtilis: the bgl gene
 RT product has both transport and reductase functions similar to those
 RT of BglF, its Escherichia coli homologue."
 RL J. Bacteriol. 177:1527-1535(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN:168 / BGS01A1;
 RC MEDLINE:95219089; PubMed:7704263;
 RC Yoshida K., et al., Sano H., Seki S., et al., F. J. Biol. Sci.
 RT "Cloning and sequencing of a 29 kb region of the Bacillus subtilis
 RT genome containing the hut and wlaA genes."
 RL Microbiology 141:47-54(1995).
 CC -1- CATALYTIC ACTIVITY: HYDROLYSIS OF TERMINAL, NON-REDUCING BETA-1-
 CC GLUCOSE RESIDUES WITH RELEASE OF BETA-D-GLUCOSE
 CC -1- SIMILARITY: BELONGS TO FAMILY 2 OF HYDROLYTIC ENZYMES
 CC
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL databank.
 CC The European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is not removed,
 CC modified and this statement is not removed, altered or used by any other
 CC entity; requires a license agreement for commercial use.
 CC or send an email to license@ebi.ac.uk

DR EMBL: Z44526; CAAB4287.1;
 DR EMBL: D31856; BAA06573.1;
 DR EMBL: D29885; BAA06573.1;
 DR EMBL: 299124; CAB1962.1; ALT_INTL
 DR PIR: S47175; S47175
 DR HSSP: P1546; IPRG

DR Subtilisin; B01993; b01H
 DR InterPro: IPR003360;
 DR Pfam: PF02142; G1Y0_HYDROL_1
 DR EMBL: F03000; EG12570; PTA
 DR EMBL: D14003; AAA97227.1; ALT_INTL
 DR EMBL: AF00503; AAC77287.1; ALT_INTL
 DR F03000; EG12570; PTA
 DR InterPro: IPR002745
 DR Pfam: PF01853; D0F603.1
 DR Transferrase; MAD
 SQ SEQUENCE 409 AA: 53289 MW: 406348.772E+04 180664

Query Match: 57.6%; Score 381; ID 1; Length 409
 Best Local Similarity 54.5%; Prod. No. 74
 Matches 6; Conservative 4; Mismatch 1; Indels 0; Gaps 0

QY 2 ALG1NPGCW 12
 I:11:1111
 DP 114 LALVNRVYKWK 144

RESULT 13
 TAE_HUMAN
 ID TAE_HUMAN STANDARD: PRI: 100 AA
 AC Q9UJ10;
 DT 01-OCT-2000 (rel. 49, Created)
 DI 01-OCT-2000 (rel. 49, Last sequence update)
 DT 01-OCT-2000 (rel. 49, Last annotation update)
 DE TAEH1N DEPTIN N-TERMINAL (HUMAN) (HUMAN)
 GN TAEH1N OR TAEH1N
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Gnathostomata; Vertebrata; Mammalia
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
 OX NCBI_TaxID:9606
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE:2009497; PubMed:10420814
 RA Chang P., Stoenen T.
 RX "Deletion of the epsilon-tubulin gene from the mouse genome
 RT reveals new aspects of epsilon-tubulin structure and function."
 RL Nat. Cell Biol. 2:340-39(2000).
 CC -1- SURFACEDOMAIN LOCATION: MEMBRANE ASSOCIATED WITH PERCENTRULAST
 CC MATERIAL
 CC -1- SIMILARITY: BELONGS TO THE TAEH1N FAMILY
 CC
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL databank.
 CC The European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is not removed,
 CC modified and this statement is not removed, altered or used by any other
 CC entity; requires a license agreement for commercial use.
 CC or send an email to license@ebi.ac.uk

DR EMBL: AF20144; AAF09545.1;
 DR Microbiology; GTPase-binding
 DR NP 0101 144 154 GTPase-binding
 DR SEQUENCE 475 AA: 52931 MW: 49977.700AF00 00004

Query Match: 57.6%; Score 381; ID 1; Length 475
 Best Local Similarity 100.0%; Prod. No. 74
 Matches 6; Conservative 4; Mismatch 0; Indels 0; Gaps 0

QY 3 LALVNRVYKWK 12
 I:11:1111
 DP 376 NQDQKWK 481

RESULT 14
 Y018_YEAST
 ID Y018_YEAST STANDARD: PRI: 100 AA
 AC P54207;



Genome version 1.5
Copyright (c) 1994 - 2000, Cogenex Ltd.

OM protein - protein search, using SW-MBL

Run on: August 22, 2001, 11:24:58 (with 4.1m of RAM)

(without alignment)

Title:

US-08-659-254-2

Perfect score:

1429

Sequence:

1 MVLATKLVNGEYVHMSAP... (VLDL...)

Scoring table:

Gap: 10.0, Gapext: 0.5

Total number of hits satisfying chosen parameters: 107339

Minimum DB seq length: 0

Maximum DB seq length: 2006000000

Post processing: Minimum Match: 08

Listing first 45 summaries

Database:

Issued_Patents_AA*

1: 1002 1002 1002 1002 1002 1002 1002 1002 1002 1002
2: 1002 1002 1002 1002 1002 1002 1002 1002 1002 1002
3: 1002 1002 1002 1002 1002 1002 1002 1002 1002 1002
4: 1002 1002 1002 1002 1002 1002 1002 1002 1002 1002
5: 1002 1002 1002 1002 1002 1002 1002 1002 1002 1002
6: 1002 1002 1002 1002 1002 1002 1002 1002 1002 1002

Pred. No. is the number of results identified by chance to have a score greater than or equal to the score of the result being reported, and is derived by analysis of the hit score distribution.

Summary:

Result No.	Score	Query Match	Length	DB ID	Accession
1	1429	100.0	284	US-08-659-254-2	Sequence 2, Aff1
2	1429	100.0	284	US-08-659-254-2	Sequence 18, Aff1
3	1256.5	88.1	285	US-08-659-254-15	Sequence 2, Aff1
4	1252.5	87.6	285	US-08-659-254-15	Sequence 18, Aff1
5	374	25.2	415	US-08-659-254-15	Sequence 2, Aff1
6	103	7.2	19	US-08-659-254-15	Sequence 18, Aff1
7	103	7.2	19	US-08-659-254-15	Sequence 2, Aff1
8	99.5	7.0	291	US-08-659-254-15	Sequence 18, Aff1
9	96.5	6.8	276.3	US-08-659-254-15	Sequence 2, Aff1
10	92	6.4	527	US-08-659-254-15	Sequence 18, Aff1
11	87.5	6.1	255	US-08-659-254-15	Sequence 2, Aff1
12	87.5	6.1	255	US-08-659-254-15	Sequence 18, Aff1
13	83	5.8	553	US-08-659-254-15	Sequence 2, Aff1
14	80	5.6	14	US-08-659-254-15	Sequence 18, Aff1
15	80	5.6	14	US-08-659-254-15	Sequence 2, Aff1
16	80	5.6	14	US-08-659-254-15	Sequence 18, Aff1
17	80	5.6	14	US-08-659-254-15	Sequence 2, Aff1
18	79.5	5.6	222	US-08-659-254-15	Sequence 18, Aff1
19	79.5	5.6	222	US-08-659-254-15	Sequence 2, Aff1
20	78.5	5.5	572	US-08-659-254-15	Sequence 18, Aff1
21	78.5	5.5	572	US-08-659-254-15	Sequence 2, Aff1
22	77	5.4	213	US-08-659-254-15	Sequence 18, Aff1
23	77	5.4	244	US-08-659-254-15	Sequence 2, Aff1
24	76.5	5.4	434	US-08-659-254-15	Sequence 18, Aff1
25	76.5	5.4	573	US-08-659-254-15	Sequence 2, Aff1
26	76.5	5.4	573	US-08-659-254-15	Sequence 18, Aff1
27	75.5	5.3	765	US-08-659-254-15	Sequence 2, Aff1

28	75	5.2	600	US-08-659-254-15	Sequence 2, Aff1
29	75	5.2	600	US-08-659-254-15	Sequence 18, Aff1
30	75	5.2	614	US-08-659-254-15	Sequence 2, Aff1
31	75	5.2	614	US-08-659-254-15	Sequence 18, Aff1
32	75	5.2	614	US-08-659-254-15	Sequence 2, Aff1
33	75	5.2	614	US-08-659-254-15	Sequence 18, Aff1
34	75	5.2	614	US-08-659-254-15	Sequence 2, Aff1
35	75	5.2	614	US-08-659-254-15	Sequence 18, Aff1
36	75	5.2	614	US-08-659-254-15	Sequence 2, Aff1
37	75	5.2	614	US-08-659-254-15	Sequence 18, Aff1
38	75	5.2	614	US-08-659-254-15	Sequence 2, Aff1
39	74.5	5.2	614	US-08-659-254-15	Sequence 18, Aff1
40	74.5	5.2	614	US-08-659-254-15	Sequence 2, Aff1
41	74.5	5.2	614	US-08-659-254-15	Sequence 18, Aff1
42	74	5.2	614	US-08-659-254-15	Sequence 2, Aff1
43	74	5.2	614	US-08-659-254-15	Sequence 18, Aff1
44	74	5.2	614	US-08-659-254-15	Sequence 2, Aff1
45	74	5.2	614	US-08-659-254-15	Sequence 18, Aff1

ALL INFORMATION CONTAINED HEREIN IS UNCLASSIFIED

RESULT 1
US-08-659-254-2
Sequence 2, Aff1
Patent No. 6104155
GENERAL INFORMATION:
APPLICANT: Cogenex, Douglas M.
INVENTOR: Cogenex, Douglas M.
TITLE: Amino acid
STATE: TX
COUNTRY: U.S.A.
ZIP: 75201
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patented Release 1.1
CURRENT APPLICATION DATA:
APPLICANT: Cogenex
FILING DATE: 07-JUN-1996
CLASSIFICATION: 530
PUBLICATION: 03-08-1997
APPLICATION NUMBER: 03-08-1997
FILING DATE: 04-01-1995
APPLICANT: Cogenex
NAME: Mayfield, Douglas L.
REGISTRATION NUMBER: 44,772
TITLE: Amino acid
TELEPHONE: 1-214-999-6290
TELEFAX: 1-214-999-6290
INVENTOR: Cogenex
SEQUENCE CHARACTERISTICS:
LENGTH: 284 amino acids
TYPE: amino acid
STRAND: Single
PROPERTY: Linear
MOLECULE TYPE: protein
US-08-659-254-2

Query Match: 100.0% (284/284)
Best Local Similarity: 100.0% (284/284)
Matrix: 276, 100.0% (284/284)

ALL INFORMATION CONTAINED HEREIN IS UNCLASSIFIED

DATE 08-08-01 BY 6032

REASON FOR DECLASSIFICATION: 25X(1) (b) (7) (D)

DATE OF REVIEW: 08/08/01

REVIEWER: [REDACTED]

APPROVAL: [REDACTED]

DATE OF REVIEW: 08/08/01

REVIEWER: [REDACTED]

APPROVAL: [REDACTED]

DATE OF REVIEW: 08/08/01

REVIEWER: [REDACTED]

APPROVAL: [REDACTED]

DATE OF REVIEW: 08/08/01

REVIEWER: [REDACTED]

APPROVAL: [REDACTED]

DATE OF REVIEW: 08/08/01

REVIEWER: [REDACTED]

APPROVAL: [REDACTED]

DATE OF REVIEW: 08/08/01

REVIEWER: [REDACTED]

APPROVAL: [REDACTED]

DATE OF REVIEW: 08/08/01

REVIEWER: [REDACTED]

APPROVAL: [REDACTED]

DATE OF REVIEW: 08/08/01

REVIEWER: [REDACTED]

APPROVAL: [REDACTED]

DATE OF REVIEW: 08/08/01

REVIEWER: [REDACTED]

APPROVAL: [REDACTED]

DATE OF REVIEW: 08/08/01

REVIEWER: [REDACTED]

APPROVAL: [REDACTED]

DATE OF REVIEW: 08/08/01

REVIEWER: [REDACTED]

APPROVAL: [REDACTED]

DATE OF REVIEW: 08/08/01

REVIEWER: [REDACTED]

APPROVAL: [REDACTED]

DATE OF REVIEW: 08/08/01

REVIEWER: [REDACTED]

APPROVAL: [REDACTED]

DATE OF REVIEW: 08/08/01

REVIEWER: [REDACTED]

APPROVAL: [REDACTED]

DATE OF REVIEW: 08/08/01

REVIEWER: [REDACTED]

APPROVAL: [REDACTED]

DATE OF REVIEW: 08/08/01

REVIEWER: [REDACTED]

APPROVAL: [REDACTED]

DATE OF REVIEW: 08/08/01

REVIEWER: [REDACTED]

APPROVAL: [REDACTED]

DATE OF REVIEW: 08/08/01

REVIEWER: [REDACTED]

APPROVAL: [REDACTED]

DATE OF REVIEW: 08/08/01

REVIEWER: [REDACTED]

APPROVAL: [REDACTED]

DATE OF REVIEW: 08/08/01

[illegible]

100-45-200-4
 Department of Agriculture
 Field No. 70241
 GENERAL INFORMATION
 APPROVAL: FALCON
 APPROVAL: N. L. V.

[illegible][illegible]

[illegible]

GenCode Version 1.2
Copyright 1993-1995, 1997, 1998, 1999, 2000, 2001

OM protein - protein search, using sw model

Run on: August 22, 2001, 14:29:09

Search time: 101.00 seconds
(81 hours of computer time)
7.145 Million cell operations/s

Title: US-08-659-254-4

Perfect score: 66

Sequence: 1 AUA11NDEGWR 12

Scoring table: BLOSUM62

Gapopen: 10.0, Gapext: 0.5

Search: 412575 seqs, 60624989 total hits

Total number of hits satisfying chosen parameters: 11,676

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match: 0%

Maximum Match: 100%

Listing first 45 results:

Result No.	Score	Query Match	Length	DB ID	Accession
1	66	100.0	12	20	AAW74156
2	66	100.0	12	22	AAW74157
3	66	100.0	284	20	AAW74158
4	66	100.0	294	22	AAW74159
5	61	92.4	284	17	AAW74160
6	61	92.4	285	17	AAW74161
7	61	92.4	285	17	AAW74162
8	61	92.4	285	17	AAW74163
9	61	92.4	285	17	AAW74164
10	61	92.4	285	17	AAW74165
11	61	92.4	285	17	AAW74166

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being returned, and is derived by analysis of the raw score distribution.

SI MMAR 2.5

12	61	92.4	285	22	AAW74168	Human Steroidogenic Acyl-CoA oxidase 1
13	52	78.8	11	22	AAW74169	Human Steroidogenic Acyl-CoA oxidase 2
14	48	71.4	8.4	22	AAW74170	Human Steroidogenic Acyl-CoA oxidase 3
15	43	65.2	800	8	AAW74171	Human Steroidogenic Acyl-CoA oxidase 4
16	43	65.2	822	18	AAW74172	Human Steroidogenic Acyl-CoA oxidase 5
17	39	59.1	446	21	AAW74173	Human Steroidogenic Acyl-CoA oxidase 6
18	38	57.6	132	20	AAW74174	Human Steroidogenic Acyl-CoA oxidase 7
19	38	57.6	132	20	AAW74175	Human Steroidogenic Acyl-CoA oxidase 8
20	38	57.6	132	20	AAW74176	Human Steroidogenic Acyl-CoA oxidase 9
21	38	57.6	132	20	AAW74177	Human Steroidogenic Acyl-CoA oxidase 10
22	38	57.6	132	20	AAW74178	Human Steroidogenic Acyl-CoA oxidase 11
23	37	56.1	93	21	AAW74179	Human Steroidogenic Acyl-CoA oxidase 12
24	37	56.1	93	21	AAW74180	Human Steroidogenic Acyl-CoA oxidase 13
25	37	56.1	113	21	AAW74181	Human Steroidogenic Acyl-CoA oxidase 14
26	37	56.1	140	21	AAW74182	Human Steroidogenic Acyl-CoA oxidase 15
27	37	56.1	140	21	AAW74183	Human Steroidogenic Acyl-CoA oxidase 16
28	37	56.1	140	21	AAW74184	Human Steroidogenic Acyl-CoA oxidase 17
29	37	56.1	140	21	AAW74185	Human Steroidogenic Acyl-CoA oxidase 18
30	37	56.1	140	21	AAW74186	Human Steroidogenic Acyl-CoA oxidase 19
31	37	56.1	140	21	AAW74187	Human Steroidogenic Acyl-CoA oxidase 20
32	37	56.1	140	21	AAW74188	Human Steroidogenic Acyl-CoA oxidase 21
33	37	56.1	140	21	AAW74189	Human Steroidogenic Acyl-CoA oxidase 22
34	37	56.1	140	21	AAW74190	Human Steroidogenic Acyl-CoA oxidase 23
35	37	56.1	140	21	AAW74191	Human Steroidogenic Acyl-CoA oxidase 24
36	37	56.1	140	21	AAW74192	Human Steroidogenic Acyl-CoA oxidase 25
37	37	56.1	140	21	AAW74193	Human Steroidogenic Acyl-CoA oxidase 26
38	37	56.1	140	21	AAW74194	Human Steroidogenic Acyl-CoA oxidase 27
39	37	56.1	140	21	AAW74195	Human Steroidogenic Acyl-CoA oxidase 28
40	37	56.1	140	21	AAW74196	Human Steroidogenic Acyl-CoA oxidase 29
41	37	56.1	140	21	AAW74197	Human Steroidogenic Acyl-CoA oxidase 30
42	37	56.1	140	21	AAW74198	Human Steroidogenic Acyl-CoA oxidase 31
43	37	56.1	140	21	AAW74199	Human Steroidogenic Acyl-CoA oxidase 32
44	37	56.1	140	21	AAW74200	Human Steroidogenic Acyl-CoA oxidase 33
45	37	56.1	140	21	AAW74201	Human Steroidogenic Acyl-CoA oxidase 34
46	37	56.1	140	21	AAW74202	Human Steroidogenic Acyl-CoA oxidase 35
47	37	56.1	140	21	AAW74203	Human Steroidogenic Acyl-CoA oxidase 36
48	37	56.1	140	21	AAW74204	Human Steroidogenic Acyl-CoA oxidase 37
49	37	56.1	140	21	AAW74205	Human Steroidogenic Acyl-CoA oxidase 38
50	37	56.1	140	21	AAW74206	Human Steroidogenic Acyl-CoA oxidase 39
51	37	56.1	140	21	AAW74207	Human Steroidogenic Acyl-CoA oxidase 40
52	37	56.1	140	21	AAW74208	Human Steroidogenic Acyl-CoA oxidase 41
53	37	56.1	140	21	AAW74209	Human Steroidogenic Acyl-CoA oxidase 42
54	37	56.1	140	21	AAW74210	Human Steroidogenic Acyl-CoA oxidase 43
55	37	56.1	140	21	AAW74211	Human Steroidogenic Acyl-CoA oxidase 44
56	37	56.1	140	21	AAW74212	Human Steroidogenic Acyl-CoA oxidase 45
57	37	56.1	140	21	AAW74213	Human Steroidogenic Acyl-CoA oxidase 46
58	37	56.1	140	21	AAW74214	Human Steroidogenic Acyl-CoA oxidase 47
59	37	56.1	140	21	AAW74215	Human Steroidogenic Acyl-CoA oxidase 48
60	37	56.1	140	21	AAW74216	Human Steroidogenic Acyl-CoA oxidase 49
61	37	56.1	140	21	AAW74217	Human Steroidogenic Acyl-CoA oxidase 50
62	37	56.1	140	21	AAW74218	Human Steroidogenic Acyl-CoA oxidase 51
63	37	56.1	140	21	AAW74219	Human Steroidogenic Acyl-CoA oxidase 52
64	37	56.1	140	21	AAW74220	Human Steroidogenic Acyl-CoA oxidase 53
65	37	56.1	140	21	AAW74221	Human Steroidogenic Acyl-CoA oxidase 54
66	37	56.1	140	21	AAW74222	Human Steroidogenic Acyl-CoA oxidase 55
67	37	56.1	140	21	AAW74223	Human Steroidogenic Acyl-CoA oxidase 56
68	37	56.1	140	21	AAW74224	Human Steroidogenic Acyl-CoA oxidase 57
69	37	56.1	140	21	AAW74225	Human Steroidogenic Acyl-CoA oxidase 58
70	37	56.1	140	21	AAW74226	Human Steroidogenic Acyl-CoA oxidase 59
71	37	56.1	140	21	AAW74227	Human Steroidogenic Acyl-CoA oxidase 60
72	37	56.1	140	21	AAW74228	Human Steroidogenic Acyl-CoA oxidase 61
73	37	56.1	140	21	AAW74229	Human Steroidogenic Acyl-CoA oxidase 62
74	37	56.1	140	21	AAW74230	Human Steroidogenic Acyl-CoA oxidase 63
75	37	56.1	140	21	AAW74231	Human Steroidogenic Acyl-CoA oxidase 64
76	37	56.1	140	21	AAW74232	Human Steroidogenic Acyl-CoA oxidase 65
77	37	56.1	140	21	AAW74233	Human Steroidogenic Acyl-CoA oxidase 66
78	37	56.1	140	21	AAW74234	Human Steroidogenic Acyl-CoA oxidase 67
79	37	56.1	140	21	AAW74235	Human Steroidogenic Acyl-CoA oxidase 68
80	37	56.1	140	21	AAW74236	Human Steroidogenic Acyl-CoA oxidase 69
81	37	56.1	140	21	AAW74237	Human Steroidogenic Acyl-CoA oxidase 70
82	37	56.1	140	21	AAW74238	Human Steroidogenic Acyl-CoA oxidase 71
83	37	56.1	140	21	AAW74239	Human Steroidogenic Acyl-CoA oxidase 72
84	37	56.1	140	21	AAW74240	Human Steroidogenic Acyl-CoA oxidase 73
85	37	56.1	140	21	AAW74241	Human Steroidogenic Acyl-CoA oxidase 74
86	37	56.1	140	21	AAW74242	Human Steroidogenic Acyl-CoA oxidase 75
87	37	56.1	140	21	AAW74243	Human Steroidogenic Acyl-CoA oxidase 76
88	37	56.1	140	21	AAW74244	Human Steroidogenic Acyl-CoA oxidase 77
89	37	56.1	140	21	AAW74245	Human Steroidogenic Acyl-CoA oxidase 78
90	37	56.1	140	21	AAW74246	Human Steroidogenic Acyl-CoA oxidase 79
91	37	56.1	140	21	AAW74247	Human Steroidogenic Acyl-CoA oxidase 80
92	37	56.1	140	21	AAW74248	Human Steroidogenic Acyl-CoA oxidase 81
93	37	56.1	140	21	AAW74249	Human Steroidogenic Acyl-CoA oxidase 82
94	37	56.1	140	21	AAW74250	Human Steroidogenic Acyl-CoA oxidase 83
95	37	56.1	140	21	AAW74251	Human Steroidogenic Acyl-CoA oxidase 84
96	37	56.1	140	21	AAW74252	Human Steroidogenic Acyl-CoA oxidase 85
97	37	56.1	140	21	AAW74253	Human Steroidogenic Acyl-CoA oxidase 86
98	37	56.1	140	21	AAW74254	Human Steroidogenic Acyl-CoA oxidase 87
99	37	56.1	140	21	AAW74255	Human Steroidogenic Acyl-CoA oxidase 88
100	37	56.1	140	21	AAW74256	Human Steroidogenic Acyl-CoA oxidase 89



SEQUENCE CHARACTERISTICS:
 LENGTH: 264 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-659-960-2

Query Match 100.0% Score 6.18 E-27 Length 264
 Best Local Similarity 100.0% Prot. No. 0.0017
 Matches 12 Conservative 02 Missed 008 00 Gaps 0

QY 1 ALGHN:DPWK 12
 DI 85 ALGHN:DPWK 96

RESULT 5
 US-08-410-540-2
 Sequence 2: Application US/09119540
 Patent No. 5407492

GENERAL INFORMATION:
 APPLICANT: Miller, Walter L.
 APPLICANT: Strauss III, Jerome F.
 TITLE OF INVENTION: IDENTIFICATION OF AN AGENT IN
 TITLE OF INVENTION: IDENTIFICATION WITH A GENERAL AGENT
 NUMBER OF SEQUENCES: 10
 CORRESPONDENCE ADDRESS:
 ADDRESS: 5 Palo Alto Square
 STREET: 5 Palo Alto Square
 CITY: Palo Alto
 STATE: CA
 COUNTRY: US
 ZIP: 94306-2155

COMPUTER RELEVABLE FORM:
 MEDIUM TYPE: floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC DOS/MS DOS
 SOFTWARE: Patent In Release #1.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: 09/09119540
 FILING DATE: 23-MAR-1995
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Nepley, Richard L.
 REGISTRATION NUMBER: 30,092
 PAPERWORK: PFT RTMAGE 0001 2 000000

TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415 853 5070

TELEFAX: 415 857 0663
 TELEX: 180816COOLEYPA

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:
 LENGTH: 265 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-410-540-2

Query Match 92.4% Score 6.18 E-27 Length 265
 Best Local Similarity 91.7% Prot. No. 0.0017
 Matches 11 Conservative 1 Missed 008 00 Gaps 0

QY 1 ALGHN:DPWK 12
 DI 86 ALGHN:DPWK 97

RESULT 5
 US-08-659-254-14

Sequence 18: Application US/09650254
 Patent No. 6194565

GENERAL INFORMATION:
 APPLICANT: Shorco, Douglas M.
 APPLICANT: Plack, Dr. Barbara J.
 TITLE OF INVENTION: COMPOSITION AND METHODS FOR
 TITLE OF INVENTION: COMPOSITION AND METHODS FOR
 NUMBER OF SEQUENCES: 19
 CORRESPONDENCE ADDRESS:
 ADDRESS: 2815 Gung, Strauss, Lane & Co. 1111
 STREET: Two Frost Bank Plaza 2000 2000
 CITY: Austin
 STATE: TX

COUNTRY: USA
 ZIP: 78701

COMPUTER RELEVABLE FORM:
 MEDIUM TYPE: floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC DOS/MS DOS
 SOFTWARE: Patent In Release #1.0

GENERAL INFORMATION:
 APPLICATION NUMBER: US 08/938,966
 FILING DATE: 04-01-1995
 CLASSIFICATION: 530
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/938,966

ATTORNEY/AGENT INFORMATION:
 NAME: Maffei, Douglas L.
 REGISTRATION NUMBER: 31,712
 PAPERWORK: PFT RTMAGE 0001 2 000000
 TELEPHONE: 512/499-6200
 TELEFAX: 512/499-6200

INFORMATION FOR SEQ ID NO: 18:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 265 amino acids
 TYPE: amino acid
 TOPOLOGY: linear

US-08-659-254-14

Query Match 92.4% Score 6.18 E-27 Length 265
 Best Local Similarity 91.7% Prot. No. 0.0017
 Matches 11 Conservative 1 Missed 008 00 Gaps 0

QY 1 ALGHN:DPWK 12
 DI 86 ALGHN:DPWK 97

RESULT 7
 US-08-538-960-8

Sequence 8: Application US/08538960
 Patent No. 5872240

GENERAL INFORMATION:
 APPLICANT: Shorco, Douglas M.
 APPLICANT: Plack, Barbara J.
 TITLE OF INVENTION: COMPOSITION AND METHODS FOR
 TITLE OF INVENTION: COMPOSITION AND METHODS FOR
 NUMBER OF SEQUENCES: 14
 CORRESPONDENCE ADDRESS:
 ADDRESS: 2815 Gung, Strauss, Lane & Co. 1111
 STREET: Two Frost Bank Plaza 2000 2000
 CITY: Austin
 STATE: TX

COUNTRY: USA
 ZIP: 78701

COMPUTER RELEVABLE FORM:
 MEDIUM TYPE: floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC DOS/MS DOS
 SOFTWARE: Patent In Release #1.0

US-08-538-960-8

1 NUMBER OF SEQUENCES: 19
 2 CORRESPONDENCE ADDRESS:
 3 ADDRESS: ABLO, GUY, ST11333, IL 606 6 FILL, 11111
 4 STREET 1400 Press Road Plaza, 11111, 11111
 5 CITY: Austin
 6 STATE: TX
 7 COUNTRY: U.S.A.
 8 ZIP: 78701
 9 COMPUTER READABLE FORM:
 10 MEDIUM TYPE: floppy disk
 11 COMPUTER: IBM PC compatible
 12 OPERATING SYSTEM: PC-DOS/MS-DOS
 13 SOFTWARE: Patent In Release #1.1, Vol. 00 #1.30
 14 CURRENT APPLICATION DATA:
 15 APPLICATION NUMBER: US/88/059,054
 16 FILING DATE: 07-JUN-1996
 17 CLASSIFICATION: 530
 18 PRIORITY APPLICATION DATA:
 19 APPLICATION NUMBER: US 08/538,066
 20 FILING DATE: 04-OCT-1995
 21 ATTORNEY/AGENT INFORMATION:
 22 NAME: Mayfield, Denise L.
 23 REGISTRATION NUMBER: 43,732
 24 REFERENCE/WORKSHEET NUMBER: 4375 000
 25 TELECOMMUNICATION INFORMATION:
 26 TELEPHONE: 512/499-6200
 27 TELEFAX: 512/499-6290
 28 INFORMATION FOR SEQ ID NO: 6:
 29 SEQUENCE CHARACTERISTICS:
 30 LENGTH: 6 amino acids
 31 TYPE: amino acid
 32 STRANDNESS: single
 33 TOPOLOGY: linear
 34 MOLECULE TYPE: peptide
 35 US-08-659-254-6

1 Query Match 57.6% Score 40 DB 42 Length 6
 2 Post Local Similarity 100.0% Pct. N. 1.4e-05
 3 Matches 62 Query 100 02 M seq 1000 02 0000 02 0000
 4
 5 QY 7 NCPKWK 12
 6 111111
 7 DB 1 NCPKWK 6
 8
 9 RESULT 11
 10 US-09-026-587-3
 11 Sequence 3, Application US/09/05507
 12 Patent No. 5912128
 13 GENERAL INFORMATION:
 14 APPLICANT: Lal, Preeti
 15 APPLICANT: Gagliardi, Karl J.
 16 APPLICANT: Gurley, Neil C.
 17 TITLE OF INVENTION: PPMAN PMA VAPOR PMA PMA
 18 NUMBER OF SEQUENCES: 4
 19 CORRESPONDENCE ADDRESS:
 20 ADDRESSEE: Incyte Pharmaceuticals, Inc.
 21 STREET: 3174 Porter Drive
 22 CITY: Palo Alto
 23 STATE: CA
 24 COUNTRY: USA
 25 ZIP: 94304
 26 COMPUTER READABLE FORM:
 27 MEDIUM TYPE: diskette
 28 COMPUTER: IBM compatible
 29 OPERATING SYSTEM: DOS
 30 SOFTWARE: FASTSEQ for Windows Version 2.0
 31 CURRENT APPLICATION DATA:
 32 APPLICATION NUMBER: US/09/026-587
 33 FILING DATE: Filed Herewith
 34 CLASSIFICATION:
 35 PRIORITY APPLICATION DATA:

1 APPLICATION NUMBER:
 2 FILING DATE:
 3 ATTORNEY/AGENT INFORMATION:
 4 NAME: Mayfield, Denise L.
 5 REGISTRATION NUMBER: 43,732
 6 REFERENCE/WORKSHEET NUMBER: 4375 000
 7 TELECOMMUNICATION INFORMATION:
 8 TELEPHONE: 512/499-6200
 9 TELEFAX: 512/499-6290
 10 PRIORITY APPLICATION DATA:
 11 APPLICATION NUMBER: US 08/538,066
 12 FILING DATE: 04-OCT-1995
 13 ATTORNEY/AGENT INFORMATION:
 14 NAME: Mayfield, Denise L.
 15 REGISTRATION NUMBER: 43,732
 16 REFERENCE/WORKSHEET NUMBER: 4375 000
 17 TELECOMMUNICATION INFORMATION:
 18 TELEPHONE: 512/499-6200
 19 TELEFAX: 512/499-6290
 20 PRIORITY APPLICATION DATA:
 21 APPLICATION NUMBER: US 08/538,066
 22 FILING DATE: 04-OCT-1995
 23 ATTORNEY/AGENT INFORMATION:
 24 NAME: Mayfield, Denise L.
 25 REGISTRATION NUMBER: 43,732
 26 REFERENCE/WORKSHEET NUMBER: 4375 000
 27 TELECOMMUNICATION INFORMATION:
 28 TELEPHONE: 512/499-6200
 29 TELEFAX: 512/499-6290
 30 PRIORITY APPLICATION DATA:

1 Query Match 56.1% Score 37 DB 42 Length 6
 2 Post Local Similarity 100.0% Pct. N. 1.4e-05
 3 Matches 72 Query 100 02 M seq 1000 02 0000 02 0000
 4
 5 QY 1 ALCHINDR 10
 6 111111
 7 DB 108 ALCHINDR 17

1 RESULT 12
 2 US-09-227-420-3
 3 Sequence 3, Application US/09/227420
 4 Patent No. 5910092
 5 GENERAL INFORMATION:
 6 APPLICANT: Lal, Preeti
 7 APPLICANT: Gagliardi, Karl J.
 8 APPLICANT: Gurley, Neil C.
 9 TITLE OF INVENTION: PPMAN PMA VAPOR PMA PMA
 10 NUMBER OF SEQUENCES: 4
 11 CORRESPONDENCE ADDRESS:
 12 ADDRESSEE: Incyte Pharmaceuticals, Inc.
 13 STREET: 3174 Porter Drive
 14 CITY: Palo Alto
 15 STATE: CA
 16 COUNTRY: USA
 17 ZIP: 94304
 18 COMPUTER READABLE FORM:
 19 MEDIUM TYPE: diskette
 20 COMPUTER: IBM compatible
 21 OPERATING SYSTEM: DOS
 22 SOFTWARE: FASTSEQ for Windows Version 2.0
 23 CURRENT APPLICATION DATA:
 24 APPLICATION NUMBER: US/09/227-420
 25 FILING DATE: Filed Herewith
 26 CLASSIFICATION:
 27 PRIORITY APPLICATION DATA:
 28 APPLICATION NUMBER: US/09/227-420
 29 FILING DATE: Filed Herewith
 30 ATTORNEY/AGENT INFORMATION:
 31 NAME: Mayfield, Denise L.
 32 REGISTRATION NUMBER: 43,732
 33 REFERENCE/WORKSHEET NUMBER: 4375 000
 34 TELECOMMUNICATION INFORMATION:
 35 TELEPHONE: 512/499-6200
 36 TELEFAX: 512/499-6290
 37 PRIORITY APPLICATION DATA:
 38 APPLICATION NUMBER: US 08/538,066
 39 FILING DATE: 04-OCT-1995
 40 ATTORNEY/AGENT INFORMATION:
 41 NAME: Mayfield, Denise L.
 42 REGISTRATION NUMBER: 43,732
 43 REFERENCE/WORKSHEET NUMBER: 4375 000
 44 TELECOMMUNICATION INFORMATION:
 45 TELEPHONE: 512/499-6200
 46 TELEFAX: 512/499-6290
 47 PRIORITY APPLICATION DATA:

IDENTIFICATION
IMPERIAL SOURCE
LIBRARY: 1000000000
NAME: 1000000000
1000000000

IDENTIFICATION
IMPERIAL SOURCE
LIBRARY: 1000000000
NAME: 1000000000
1000000000

IDENTIFICATION
IMPERIAL SOURCE
LIBRARY: 1000000000
NAME: 1000000000
1000000000

IDENTIFICATION
IMPERIAL SOURCE
LIBRARY: 1000000000
NAME: 1000000000
1000000000

IDENTIFICATION
IMPERIAL SOURCE
LIBRARY: 1000000000
NAME: 1000000000
1000000000

IDENTIFICATION
IMPERIAL SOURCE
LIBRARY: 1000000000
NAME: 1000000000
1000000000

IDENTIFICATION
IMPERIAL SOURCE
LIBRARY: 1000000000
NAME: 1000000000
1000000000

IDENTIFICATION
IMPERIAL SOURCE
LIBRARY: 1000000000
NAME: 1000000000
1000000000

IDENTIFICATION
IMPERIAL SOURCE
LIBRARY: 1000000000
NAME: 1000000000
1000000000

IDENTIFICATION
IMPERIAL SOURCE
LIBRARY: 1000000000
NAME: 1000000000
1000000000

IDENTIFICATION
IMPERIAL SOURCE
LIBRARY: 1000000000
NAME: 1000000000
1000000000

IDENTIFICATION
IMPERIAL SOURCE
LIBRARY: 1000000000
NAME: 1000000000
1000000000

IDENTIFICATION
IMPERIAL SOURCE
LIBRARY: 1000000000
NAME: 1000000000
1000000000

IDENTIFICATION
IMPERIAL SOURCE
LIBRARY: 1000000000
NAME: 1000000000
1000000000

IDENTIFICATION
IMPERIAL SOURCE
LIBRARY: 1000000000
NAME: 1000000000
1000000000

IDENTIFICATION
IMPERIAL SOURCE
LIBRARY: 1000000000
NAME: 1000000000
1000000000

IDENTIFICATION
IMPERIAL SOURCE
LIBRARY: 1000000000
NAME: 1000000000
1000000000

IDENTIFICATION
IMPERIAL SOURCE
LIBRARY: 1000000000
NAME: 1000000000
1000000000

IDENTIFICATION
IMPERIAL SOURCE
LIBRARY: 1000000000
NAME: 1000000000
1000000000

IDENTIFICATION
IMPERIAL SOURCE
LIBRARY: 1000000000
NAME: 1000000000
1000000000

COUNTRY: USA
 ZIP: 98121
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FASTSEQ for Windows V-1.1.2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: 08/08/997,000
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 AGENCY/AGENCY INFORMATION:
 NAME: Sleath, Janet
 REGISTRATION NUMBER: 97,007
 REFERENCE/BOOK NUMBER: 11006,100
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 206-269-0565
 TELEFAX: 206-269-0563
 TELEX:
 INFORMATION FOR SEQ ID NO: 158:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 161 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-08-997-080-158

Query Match: 54.58; Score 0; 30 Z; Length 161
 Best Local Similarity: 66.78; Prod No. 252
 Matches: 6; Conservative: 0; M-Score: 100; 4; Models: 0; 30; 100
 QY: 4 GILNDEIN 11
 ID: 103 GILNDEIN 111

Search completed: August 22, 2001, 14:00
 Job time: 364 Sec



1. APPROXIMATELY 11:00 AM
2. APPROXIMATELY 11:00 AM

3. APPROXIMATELY 11:00 AM

4. APPROXIMATELY 11:00 AM

5. APPROXIMATELY 11:00 AM

6. APPROXIMATELY 11:00 AM

7. APPROXIMATELY 11:00 AM

8. APPROXIMATELY 11:00 AM

9. APPROXIMATELY 11:00 AM

10. APPROXIMATELY 11:00 AM

11. APPROXIMATELY 11:00 AM

12. APPROXIMATELY 11:00 AM

13. APPROXIMATELY 11:00 AM

14. APPROXIMATELY 11:00 AM

15. APPROXIMATELY 11:00 AM

16. APPROXIMATELY 11:00 AM

17. APPROXIMATELY 11:00 AM

18. APPROXIMATELY 11:00 AM

19. APPROXIMATELY 11:00 AM

20. APPROXIMATELY 11:00 AM

21. APPROXIMATELY 11:00 AM

22. APPROXIMATELY 11:00 AM

23. APPROXIMATELY 11:00 AM

24. APPROXIMATELY 11:00 AM

25. APPROXIMATELY 11:00 AM

26. APPROXIMATELY 11:00 AM

27. APPROXIMATELY 11:00 AM

28. APPROXIMATELY 11:00 AM

29. APPROXIMATELY 11:00 AM

30. APPROXIMATELY 11:00 AM

31. APPROXIMATELY 11:00 AM

32. APPROXIMATELY 11:00 AM

33. APPROXIMATELY 11:00 AM

34. APPROXIMATELY 11:00 AM

35. APPROXIMATELY 11:00 AM

36. APPROXIMATELY 11:00 AM

37. APPROXIMATELY 11:00 AM

38. APPROXIMATELY 11:00 AM

39. APPROXIMATELY 11:00 AM

40. APPROXIMATELY 11:00 AM

41. APPROXIMATELY 11:00 AM

42. APPROXIMATELY 11:00 AM

43. APPROXIMATELY 11:00 AM

44. APPROXIMATELY 11:00 AM

45. APPROXIMATELY 11:00 AM

46. APPROXIMATELY 11:00 AM

47. APPROXIMATELY 11:00 AM

48. APPROXIMATELY 11:00 AM

49. APPROXIMATELY 11:00 AM

50. APPROXIMATELY 11:00 AM

51. APPROXIMATELY 11:00 AM

52. APPROXIMATELY 11:00 AM

53. APPROXIMATELY 11:00 AM

54. APPROXIMATELY 11:00 AM

55. APPROXIMATELY 11:00 AM

56. APPROXIMATELY 11:00 AM

57. APPROXIMATELY 11:00 AM

58. APPROXIMATELY 11:00 AM

59. APPROXIMATELY 11:00 AM

60. APPROXIMATELY 11:00 AM

61. APPROXIMATELY 11:00 AM

62. APPROXIMATELY 11:00 AM

63. APPROXIMATELY 11:00 AM

64. APPROXIMATELY 11:00 AM

65. APPROXIMATELY 11:00 AM

66. APPROXIMATELY 11:00 AM

67. APPROXIMATELY 11:00 AM

68. APPROXIMATELY 11:00 AM

69. APPROXIMATELY 11:00 AM

70. APPROXIMATELY 11:00 AM

71. APPROXIMATELY 11:00 AM

72. APPROXIMATELY 11:00 AM

73. APPROXIMATELY 11:00 AM

74. APPROXIMATELY 11:00 AM

75. APPROXIMATELY 11:00 AM

76. APPROXIMATELY 11:00 AM

77. APPROXIMATELY 11:00 AM

78. APPROXIMATELY 11:00 AM

79. APPROXIMATELY 11:00 AM

80. APPROXIMATELY 11:00 AM

81. APPROXIMATELY 11:00 AM

82. APPROXIMATELY 11:00 AM

83. APPROXIMATELY 11:00 AM

84. APPROXIMATELY 11:00 AM

85. APPROXIMATELY 11:00 AM

86. APPROXIMATELY 11:00 AM

87. APPROXIMATELY 11:00 AM

88. APPROXIMATELY 11:00 AM

89. APPROXIMATELY 11:00 AM

90. APPROXIMATELY 11:00 AM

91. APPROXIMATELY 11:00 AM

92. APPROXIMATELY 11:00 AM

93. APPROXIMATELY 11:00 AM

94. APPROXIMATELY 11:00 AM

95. APPROXIMATELY 11:00 AM

96. APPROXIMATELY 11:00 AM

97. APPROXIMATELY 11:00 AM

98. APPROXIMATELY 11:00 AM

99. APPROXIMATELY 11:00 AM

100. APPROXIMATELY 11:00 AM

RESULTS

PPV: 0.0000

NPV: 0.0000

ACC: 0.0000

PREC: 0.0000

REC: 0.0000

F1: 0.0000

MAE: 0.0000

MAE: 0.0000

MAE: 0.0000

MAE: 0.0000

MAE: 0.0000

MAE: 0.0000

MAE: 0.0000

MAE: 0.0000

MAE: 0.0000

MAE: 0.0000

MAE: 0.0000

MAE: 0.0000

MAE: 0.0000

MAE: 0.0000

MAE: 0.0000

MAE: 0.0000

MAE: 0.0000

MAE: 0.0000

MAE: 0.0000

MAE: 0.0000

MAE: 0.0000

MAE: 0.0000

MAE: 0.0000

MAE: 0.0000

MAE: 0.0000

MAE: 0.0000

MAE: 0.0000

MAE: 0.0000

MAE: 0.0000

MAE: 0.0000

MAE: 0.0000

MAE: 0.0000

MAE: 0.0000

MAE: 0.0000

MAE: 0.0000

MAE: 0.0000

MAE: 0.0000

MAE: 0.0000

MAE: 0.0000

MAE: 0.0000

MAE: 0.0000

MAE: 0.0000

MAE: 0.0000

MAE: 0.0000

MAE: 0.0000

MAE: 0.0000

MAE: 0.0000

MAE: 0.0000

MAE: 0.0000

MAE: 0.0000

MAE: 0.0000

MAE: 0.0000

MAE: 0.0000

MAE: 0.0000

MAE: 0.0000

MAE: 0.0000

MAE: 0.0000

MAE: 0.0000

MAE: 0.0000

MAE: 0.0000

MAE: 0.0000

MAE: 0.0000

MAE: 0.0000

MAE: 0.0000

MAE: 0.0000

MAE: 0.0000

MAE: 0.0000

MAE: 0.0000

MAE: 0.0000

MAE: 0.0000

MAE: 0.0000

MAE: 0.0000

MAE: 0.0000

MAE: 0.0000

MAE: 0.0000

MAE: 0.0000

MAE: 0.0000

MAE: 0.0000

MAE: 0.0000

MAE: 0.0000

MAE: 0.0000

MAE: 0.0000

MAE: 0.0000

MAE: 0.0000

MAE: 0.0000

MAE: 0.0000

MAE: 0.0000

MAE: 0.0000


```

ID      PRLZARATH      STANJAKU      PRT: 476 AA
AC      039190:
DT      15-JUL-1998 (Rel. 36, created)
DT      15-DEC-1998 (Rel. 37, last sequence update)
DT      01-OCT-2000 (Rel. 40, last annotation update)
DE      PRLZARATH PROSRIATAS PLEIOTROPIC REG. A-OR PRLZ.
GN      PRL2.
OS      Arabidopsis thaliana (Mouse ear cress),
OC      Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC      Magnoliophyta; Eudicotyledons; Core eudicotyledons; Rosales;
OC      Brassicales; Brassicaceae; Arabidopsis.
OX      NCBI_TaxID=3702;
RN      111
RP      SEQUENCE FROM N.A.
RC      STRAIN=CV_COLUMBIA;
RX      MEDLINE 98439452; PubMed=9765207;
RA      Nemeth K., Salchert K., Putnocky P., Radovics E., Kozov K., Kumanov
RA      Stankovic-Stankovic P., Bako L., Matanovic M., Okros L., Stankovic
RA      Gedeonberger P., Stili M., Rodolich M., Stankovic J., Kozov K.;
RA      pleiotropic control of glucose and fructose responses by PRL2, a
RA      nuclear WD protein, in Arabidopsis.
RT      Genes Dev. 12:4059-4074(1998).
CC      FUNCTION: PLEIOTROPIC REGULATOR OF FRUCTOSE AND GLUCOSE RESPONSES.
CC      SIMILARITY: CONTAINS 7 WD REPEATS (IP AND ERMAMS).
CC      SIMILARITY: BELONGS TO THE PRLZARATH FAMILY OF WD REPEAT PROTEINS.
CC      This SWISS-Prot entry is copyright 1998, reproduced here for publication
CC      between the Swiss Institute of Bioinformatics and the EMBL database.
CC      The European Bioinformatics Institute, EMBL and the EMBL database are
CC      used by non-profit institutions as long as its content is in no way
CC      modified and this statement is not removed, usage by and for commercial
CC      entities requires a license agreement with the EMBL database or
CC      or send an email to license@ebi.ac.uk).
CC      EMBL: X82826; CAA58033.1;
DR      InterPro: IPR016803;
DR      Pfam: PF00400; WD40; 7;
DR      PRINTS: PR00320; GPROTEINHEAT;
DR      PROSITE: PS00678; WD_REPEATS_1; 4;
DR      PROSITE: PS00982; WD_REPEATS_2; 4;
DR      PROSITE: PS02994; WD_REPEATS_REGION; 1;
KW      Repeat; WD repeat.
FT      REPEAT 168 198  WD 1;
FT      REPEAT 210 240  WD 2;
FT      REPEAT 252 282  WD 3;
FT      REPEAT 294 324  WD 4;
FT      REPEAT 335 364  WD 5;
FT      REPEAT 477 496  WD 6;
FT      REPEAT 426 456  WD 7;
SE      SEQUENCE 479 AA; 53568 MW; 30198643FA60670180647;
Query Match: 50.0%; Score 4.0; Lp: 1; Length 479;
Best Local Similarity: 60.0%; Prev. No. 1;
Matches: 6; Conservative: 1; Mismatches: 42; Indels: 0; Gaps: 0;
QY      3 HPTGMVLLP 12
      11 1:111
ID      255 HCVYCIALLP 264

```

Search completed: August 22, 2001, 14:33:34
 Job time: 407 sec



RP SEQUENCE FROM N.A.
 RC TISSUE BRAIN, TESTIS, HEAD, KIDNEY OR N. AND LIVER
 RA GENEZ F.W.:
 RT "HAIK-1G1241330 of the HAIK-1G1241330 and HAIK-1G1241330"
 RI Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases
 DR EMBL AF282215; AM39689.1;
 SO SEQUENCE 287 AA (1884 MW) 29F AAEAL GP QPGR (16754)

Query Match 46.2% Score 531 LH 15 Length 287
 Best Local Similarity 64.7% Prot. No. 24
 Matches 92 Conservative 4 Missed bases 22 Indels 0 Gaps 0

QY 1 AERPCTVIMRHA 14
 DB 217 AERPCTVIMRHA 240

RESULT 7
 ID Q9KRG0 PRELIMINARY PRT 1 AA
 AC Q9KRG0

DI 01-MAY-2000 (TrEMBL) 13, Created
 DI 01-MAY-2000 (TrEMBL) 13, Last sequence update
 DE 01-MAR-2001 (TrEMBL) 16, Last amino acid update
 GN DR0708

OS Poliovirus radiodurans
 OC Bacteriophage Theovirus/bacteriophage group of non-enveloped, double-stranded RNA viruses
 OX NCBI_TaxID=1299

RN SEQUENCE FROM N.A.
 RC STRAIN RL

RA MEDLINE:20036896; PubMed:10567266
 RA White G., Eismann J.A., Heidelberg J., Key E.K., Peterson J.,
 RA Dodson R.L., Hart D.H., Twinn M.L., Nelson W.C., Richardson L.L.,
 RA Moffat K.S., Qin H., Jiang L., Paphitis W., Crosby M., Shao M.,
 RA Vamvakopoulos J., Lee P., Melnick J.L., Black J.A.,
 RA Makarov S., Arnold J., Bailey M.L., Wilson R.W., Finkelstein R.,
 RA Koehn V.A., Nelson J.F., et al. (2000) H. Virology 300: 1-10
 RA Foster C.M.

RT "Genomic sequence of the radiodurans bacteriophage Theovirus/bacteriophage group of non-enveloped, double-stranded RNA viruses"
 RI Science 286:1571-1577(1999)
 DR EMBL AE001927; AF10291.1;
 DR 1108; DR0708;
 DR InterPro: IP000908;
 DR PROSITE: PS00761; SPASE, L3; UNKOWN 1
 KM Hypodermal protein
 SO SEQUENCE 740 AA (78073 MW) 9AEE64 Q 00420A5 (16754)

Query Match 55.2% Score 511 LH 22 Length 240
 Best Local Similarity 88.9% Prot. No. 02
 Matches 81 Conservative 07 Missed bases 15 Indels 0 Gaps 0

QY 5 PTCVIMRHA 13
 DB 536 PTCVIMRHA 544

RESULT 8

ID Q9KRG0 PRELIMINARY PRT 1 AA
 AC Q9KRG0

DI 01-MAY-2000 (TrEMBL) 15, Created
 DI 01-MAY-2000 (TrEMBL) 15, Last sequence update
 DI 01-MAR-2001 (TrEMBL) 16, Last amino acid update
 GN DR2506 PROTEIN

OS Bacteria: halobacterium
 OC Bacteria: Firmicutes: Bacillus/ Bacillus group
 SO Bacteria/ Firmicutes group: Bacillus

OX NCBI_TaxID=999999
 RN SEQUENCE FROM N.A.
 RC STRAIN RL
 RA "HAIK-1G1241330 of the HAIK-1G1241330 and HAIK-1G1241330"
 RI Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases
 DR EMBL AF001512; F066625.1;
 SO SEQUENCE 287 AA (1884 MW) 29F AAEAL GP QPGR (16754)

Query Match 55.6% Score 511 LH 22 Length 240
 Best Local Similarity 88.9% Prot. No. 02
 Matches 81 Conservative 07 Missed bases 15 Indels 0 Gaps 0

QY 2 PTCVIMRHA 12
 DB 146 PTCVIMRHA 154

RESULT 9

ID Q9KRG0 PRELIMINARY PRT 1 AA
 AC Q9KRG0

DI 01-MAY-1999 (TrEMBL) 13, Created
 DI 01-MAY-1999 (TrEMBL) 16, Last sequence update
 DE 01-MAR-2001 (TrEMBL) 16, Last amino acid update
 GN DR0708
 OS Poliovirus radiodurans
 OC Bacteriophage Theovirus/bacteriophage group of non-enveloped, double-stranded RNA viruses
 OX NCBI_TaxID=1299

RN SEQUENCE FROM N.A.
 RC STRAIN RL
 RA MEDLINE:20036896; PubMed:10567266
 RA White G., Eismann J.A., Heidelberg J., Key E.K., Peterson J.,
 RA Dodson R.L., Hart D.H., Twinn M.L., Nelson W.C., Richardson L.L.,
 RA Moffat K.S., Qin H., Jiang L., Paphitis W., Crosby M., Shao M.,
 RA Vamvakopoulos J., Lee P., Melnick J.L., Black J.A.,
 RA Makarov S., Arnold J., Bailey M.L., Wilson R.W., Finkelstein R.,
 RA Koehn V.A., Nelson J.F., et al. (2000) H. Virology 300: 1-10
 RA Foster C.M.

RT "Large scale isolation of virus-like particles from by an improved method involving the preparation of a subviral RNA virus"
 RI Science 286:1571-1577(1999)
 DR EMBL AE001927; AF10291.1;
 DR 1108; DR0708;
 DR InterPro: IP000908;
 DR PROSITE: PS00761; SPASE, L3; UNKOWN 1
 KM Hypodermal protein
 SO SEQUENCE 740 AA (78073 MW) 9AEE64 Q 00420A5 (16754)

Query Match 54.4% Score 511 LH 22 Length 240
 Best Local Similarity 88.9% Prot. No. 02
 Matches 81 Conservative 07 Missed bases 15 Indels 0 Gaps 0

QY 1 AERPCTVIMRHA 13
 DB 217 AERPCTVIMRHA 240

RESULT 10

ID Q9KRG0 PRELIMINARY PRT 1 AA
 AC Q9KRG0

DI 01-MAY-1999 (TrEMBL) 13, Created
 DI 01-MAY-1999 (TrEMBL) 16, Last sequence update
 DI 01-MAR-2001 (TrEMBL) 16, Last amino acid update
 GN DR2506 PROTEIN
 OS Bacteria: halobacterium
 OC Bacteria: Firmicutes: Bacillus/ Bacillus group
 SO Bacteria/ Firmicutes group: Bacillus

EMBL: AE001675; AM19095.1; ...
 DB EMBL: AE002249; AF38587.1; ...
 DB TIGR: CP05011; ...
 DB InterPro: IP004029; ...
 DB Pfam: PF00575; S1; ...
 DB SOURCE: 515 AA; Genes: A7110; ...

Query Match
 Best Local Similarity 51.28; Score 41; Length 515
 Matches 6; Conservative 2; Mismatches 3; Gaps 1
 DB 453 ESHICLVHP 463

RESULT 14
 Q94S84 PRELIMINARY; PRT; ...
 AC Q94S84; ...
 PF 01-OCT-2000 (TREMUR-15, Creative)
 DE 01-OCT-2000 (TREMUR-15, Last sequence update)
 DE 01-MAR-2001 (TREMUR-15, Last sequence update)
 DE AXIAL FILAMENT PROTEIN.
 GN CAVE.
 OS Chlamydia pneumoniae (Chlamydia phylum).
 CC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
 CX MBL_TaxID=81556;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA STRAIN-318;
 RX MEDLINE=20330449; PubMed=10871462;
 RA Shirai M., Hirabayashi H., Kimoto M., Ishino M., Kishi K., ...
 RA Shiba T., Ishii K., Hattori M., Kohara S., Nakazawa T., ...
 RT *Comparison of whole genome sequences of Chlamydia pneumoniae J148
 from Japan and GW1029 from USA.*
 RL Nucleic Acids Res. 28:2411-2414 (2000).
 DB EMBL: AP002548; BAA99167.1; ...
 DB InterPro: IP004029; ...
 DB Pfam: PF00575; S1; ...
 DB SOURCE: 515 AA; Genes: A7110; ...

Query Match
 Best Local Similarity 51.28; Score 41; Length 515
 Matches 6; Conservative 2; Mismatches 3; Gaps 1

QY 2 EHGPIKCVHP 12
 11 1:1:1
 453 ESHICLVHP 463

RESULT 15
 Q94S84 PRELIMINARY; PRT; ...
 AC Q94S84; ...
 PF 01-OCT-2000 (TREMUR-15, Creative)
 DE 01-OCT-2000 (TREMUR-15, Last sequence update)
 DE 01-MAR-2001 (TREMUR-15, Last sequence update)
 DE F1504.27.
 OS Arabidopsis thaliana (Mouse-ear cress)
 CC Eukaryota; Viridiplantae; Embryophyta; Eudicotyledons; Magnoliopsida; Gentianales; Brassicales; Brassicaceae; Arabidopsis
 CX MBL_TaxID=7702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Ecker J.R.;
 RL Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Ecker J.R.;

Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Ecker J.R.;
 RL Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Ecker J.R.;

Query Match
 Best Local Similarity 51.28; Score 41; Length 515
 Matches 6; Conservative 2; Mismatches 3; Gaps 1
 DB 453 ESHICLVHP 463

Search completed August 22, 2001, 15:20:13
 Job Time: 196 Sec

Wed Aug 22 15:43:00 2001

us-08-659-254-3.rspt

Page 6

A:Residues: 1-446 <LAN>
A:Cross-references: EMBL:U63650; NID02289.01: 010-42289.01
A:Experimental source: tissue-type endothelial cells 84
C:Superfamily: 1-antimicrobial peptide 1 carbonyl de oxidase
C:Keywords: oxidoreductase

Query Match 54.1% Score 70 B at length 446
Best local Similarity 70.0% Prod No 207
Matches 77 Conserved 11 Mismat 10 S 27 Indels 1
QY 2 LSTLNNDGHW 11
1 1 1 1 1 1 1
Db 239 LQTLNPKRW 248

Search completed: August 22, 2001, 14:51:2
Job time: 79 sec



QY 160 THEIAAAGACLVCP--KPEVSEVCEK 1 274/NAH8 EHFPAAGVPAH 274
 DB 879 YGVH---KSNVHKKVYVETKRTD 1 274/NAH8 EHFPAAGVPAH 274
 QY 270 GPEGVVHFAVSEKELFWELSEKWLK 2 2
 DB 752 MSQVLETF GVS-GNSQDHCCHERNG SP4 2 2

RESULT 15

Q21140
 ID 021130 PRELIMINARY: PR3 296 W
 AC 021130:
 DT 01 NOV 1996 (JREFBUREL 01, created)
 DI 01 NOV 1996 (JREFBUREL 01, last update)
 DI 01 MAR 2001 (JREFBUREL 16, last amendment update)
 DE K0203.2, PROTEIN.
 GN K0203.2.
 OS Caenorhabditis elegans.
 OG Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae; Rhabditidae; Caenorhabditis
 OX NCBI_TaxID 62159

SEQUENCE FROM N.A.

111
 Baridill S:
 RI Submitted (MAR 1994) to the EMBL/GenBank/DBJ databases.
 RN 121
 RP SEQUENCE FROM N.A.
 RX MEDLINE:94150718; PubMed:7906398;
 RA Wilson R., Altschuld R., Anderson R., Fortes C., B. K. M.
 RA Bonfield J., Burton J., Connell M., P. J. Cooper J., G. S. A. A.
 RA Craxton M., Dear S., Du Z., Farber R., Felle A., Fulton J.,
 RA Gardner A., Green P., Hawkins J., Heston J., J. M. J. J. J. J. J.
 RA Jones M., Kershaw J., Kishen J., La S. J., La S. J., La S. J.,
 RA Litching J., Lloyd C., Murray A., Mulligan R., Mulligan R.,
 RA Parsons J., Perry S., Wilson J., Wilson J., Wilson J., Wilson J.,
 RA Smalton N., Smith A., Southam J., Southam J., Southam J.,
 RA Thierly-Miet J., Thomas K., Vaidi P., Vaidi P., Vaidi P.,
 RA Watson A., Welstock L., Wilkins-Sproul J., Wilkins-Sproul J.,
 RT * 2 Mb of contiguous nucleotide sequence from chromosome 111.2.
 RI elegans.*
 RL Mammals: 468; 32 88(1994).
 DR EMBL: Z76209; CCA94145.1;
 DR InterPro: IPR002913;
 DR Pfam: PF01852; START: 1;
 DR SMART: SM00234; START: 1;
 SO SEQUENCE 296 AA; 33485 MW; 02001744-080129-080044

Query Match

Best Local Similarity 7.18; Score: 111; DB: 100th 966;
 Lengths 37; Conservative 27; Miscellaneous 58; Indels 12; Gaps 7;

QY 145 EKNVAVETKVI GKGRT-VTHFAAAGV 1 274/NAH8 EHFPAAGVPAH 274
 DB 144 KMSQSACI SEVHSTSVTHHETGMM 1 274/NAH8 EHFPAAGVPAH 274
 QY 201 MATHEHEMPEVTEAEGECVWHP A 1 274/NAH8 EHFPAAGVPAH 274
 DB 203 SVGH EKSPRIAVVAVLITLMDP 1 274/NAH8 EHFPAAGVPAH 274
 QY 259 LNSQIIFRANHKK 272
 DB 258 MRCJASERFDLOR 271

Search completed: August 22, 2001, 14:27:
 Job Time: 194 Sec



GenCore version 1.5
Copyright (c) 1993 - 2000 Argonne Lab.

DM protein - protein search, using sw model

Run on: August 22, 2001, 14:40:29

Search time: 15.20 seconds
(without refinement)

Hit list: US-08-659-254-4

Perfect score: 80

Sequence: 1 ACHICWVHPLA 14

Scoring table: BLASTM62

Gapop: 10.0, Gapext: 0.5

Searched: 197339 seqs, 20590346 seq-bases

Total number of hits satisfying chosen parameters: 19733

Human DB seq length: 0

Human DB seq length: 2000000000

Post-processing: Minimum Match: 0%

Maximum Match: 100%

Listing list: 45 summaries

Database: Issued: Patients: AA*

1 100.0 14 2 US-08-659-254-4

2 100.0 14 4 US-08-659-254-4

3 100.0 276 2 US-08-659-254-4

4 100.0 284 2 US-08-659-254-4

5 100.0 285 1 US-08-659-254-4

6 100.0 285 4 US-08-659-254-4

7 66.2 9 4 US-08-659-254-4

8 66.2 9 4 US-08-659-254-4

9 47.5 1285 3 US-08-659-254-4

10 47.5 1285 4 US-08-659-254-4

11 47.5 1285 5 US-08-659-254-4

12 47.5 1285 6 US-08-659-254-4

13 47.5 1286 4 US-08-659-254-4

14 47.5 1299 4 US-08-659-254-4

15 46.2 215 1 US-08-659-254-4

16 46.2 716 2 US-08-659-254-4

17 46.2 716 4 US-08-659-254-4

18 46.2 4080 6 US-08-659-254-4

19 46.2 41 2 US-08-659-254-4

20 46.2 41 4 US-08-659-254-4

21 46.2 217 2 US-08-659-254-4

22 46.2 217 2 US-08-659-254-4

23 46.2 421 2 US-08-659-254-4

24 46.2 421 2 US-08-659-254-4

25 46.2 513 2 US-08-659-254-4

26 46.2 513 2 US-08-659-254-4

27 46.2 584 1 US-08-659-254-4

Prod. No. is the number of results provided by the database.
Score greater than or equal to the score of the result being filtered,
and is derived by analysis of the target score distribution.

SUMMARY

28 46.2 584 1 US-08-659-254-4
29 46.2 584 2 US-08-659-254-4
30 46.2 584 3 US-08-659-254-4
31 46.2 584 4 US-08-659-254-4
32 46.2 584 5 US-08-659-254-4
33 46.2 584 6 US-08-659-254-4
34 46.2 584 7 US-08-659-254-4
35 46.2 584 8 US-08-659-254-4
36 46.2 584 9 US-08-659-254-4
37 46.2 584 10 US-08-659-254-4
38 46.2 584 11 US-08-659-254-4
39 46.2 584 12 US-08-659-254-4
40 46.2 584 13 US-08-659-254-4
41 46.2 584 14 US-08-659-254-4
42 46.2 584 15 US-08-659-254-4
43 46.2 584 16 US-08-659-254-4
44 46.2 584 17 US-08-659-254-4
45 46.2 584 18 US-08-659-254-4

ATTACHMENTS

RESULT 1

US-08-659-254-4

Sequence: 3, Application: US/7854894

Patent: No. 5872,333

GENERAL INFORMATION:

APPLICANT: SINOVA, Douglas M.

APPLICANT: SINOVA, Douglas M.

APPLICANT: SINOVA, Douglas M.

APPLICANT: SINOVA, Douglas M.

APPLICANT: SINOVA, Douglas M.

APPLICANT: SINOVA, Douglas M.

APPLICANT: SINOVA, Douglas M.

APPLICANT: SINOVA, Douglas M.

APPLICANT: SINOVA, Douglas M.

APPLICANT: SINOVA, Douglas M.

APPLICANT: SINOVA, Douglas M.

APPLICANT: SINOVA, Douglas M.

APPLICANT: SINOVA, Douglas M.

APPLICANT: SINOVA, Douglas M.

APPLICANT: SINOVA, Douglas M.

APPLICANT: SINOVA, Douglas M.

APPLICANT: SINOVA, Douglas M.

APPLICANT: SINOVA, Douglas M.

APPLICANT: SINOVA, Douglas M.

APPLICANT: SINOVA, Douglas M.

APPLICANT: SINOVA, Douglas M.

APPLICANT: SINOVA, Douglas M.

APPLICANT: SINOVA, Douglas M.

1 NUMBER OF SEQUENCES: 19
 2 CORRESPONDENCE ADDRESS:
 3 ADDRESSEE: Peter Bobbich, Test Administration
 4 STREET: Four Embarcadero Center
 5 CITY: San Francisco
 6 STATE: CA
 7 COUNTRY: US
 8 ZIP: 94111
 9 COMPUTER READABLE FORM:
 10 MEDIUM TYPE: Floppy disk
 11 COMPUTER: IBM PC compatible
 12 OPERATING SYSTEM: PC DOS/MS DOS
 13 SOFTWARE: Patent In Release #1.0, Ver 01 #1.00
 14 CURRENT APPLICATION DATA:
 15 APPLICATION NUMBER: US/08/659,095
 16 FILING DATE:
 17 CLASSIFICATION:
 18 PRIOR APPLICATION DATA:
 19 APPLICATION NUMBER: 08/548,426
 20 FILING DATE:
 21 ATTORNEY/AGENT INFORMATION:
 22 NAME: Rowland, Bertram I
 23 REGISTRATION NUMBER: 20015
 24 REFERENCE/DOCKET NUMBER: 460196 1
 25 TELECOMMUNICATION INFORMATION:
 26 TELEPHONE: 415-781-1989
 27 TELEFAX: 415-398-8249
 28 INFORMATION FOR SEQ ID NO: 6:
 29 SEQUENCE CHARACTERISTICS:
 30 LENGTH: 1285 amino acids
 31 TYPE: amino acid
 32 STRANDEDNESS: single
 33 TOPOLOGY: linear
 34 MOLECULE TYPE: protein
 35 US-08-659-095-6
 36
 37 Query Match 47.5% Score: 48 DB: 3 Length: 1285
 38 Host Local Similarity: 58.3% Prod No: 460196
 39 Matches: 77 Conservative: 0 Mismatches: 51 Indels: 0
 40
 41 QY 3 HGTGCVLHPA 14
 42 I I I I I I
 43 DB 139 HDNNSVILHPA 150
 44
 45 RESULT 11
 46 US-08-954-668-6
 47 Sequence 6, Application: 05/0974769
 48 GENERAL INFORMATION:
 49 APPLICANT: SCOTT, MATTHEW P
 50 APPLICANT: GOODRICH, LISA V
 51 APPLICANT: JOHNSON, RONALD L
 52 TITLE OF INVENTION: Patched Genes and their use
 53 NUMBER OF SEQUENCES: 19
 54 CORRESPONDENCE ADDRESS:
 55 ADDRESSEE: Policy Road & Elliot
 56 STREET: One Post Office Square
 57 CITY: Boston
 58 STATE: MA
 59 COUNTRY: USA
 60 ZIP: 02109
 61 COMPUTER READABLE FORM:
 62 MEDIUM TYPE: Floppy disk
 63 COMPUTER: IBM PC compatible
 64 OPERATING SYSTEM: PC-DOS/MS-DOS
 65 SOFTWARE: ASCII(XXX)
 66 CURRENT APPLICATION DATA:
 67 APPLICATION NUMBER: 07/099,954 47
 68 FILING DATE: 20-Oct-1997
 69 CLASSIFICATION: 540
 70 ATTORNEY/AGENT INFORMATION:

1 NAME: Vincent, Matthew P
 2 REGISTRATION NUMBER: 96709
 3 REFERENCE/DOCKET NUMBER: 05/0974769
 4 TELECOMMUNICATION INFORMATION:
 5 TELEPHONE: 617 842-1000
 6 TELEFAX: 617 842-7000
 7 INFORMATION FOR SEQ ID NO: 6:
 8 SEQUENCE CHARACTERISTICS:
 9 LENGTH: 1285 amino acids
 10 TYPE: amino acid
 11 STRANDEDNESS: single
 12 TOPOLOGY: linear
 13 MOLECULE TYPE: protein
 14 US-08-954-668-6

Query Match 47.5% Score: 48 DB: 3 Length: 1285
 Host Local Similarity: 58.3% Prod No: 460196
 Matches: 77 Conservative: 0 Mismatches: 51 Indels: 0

QY 3 HGTGCVLHPA 14

I I I I I I

DB 139 HDNNSVILHPA 150

RESULT 12
 US-059-13233-6
 Sequence 6, Application: 05/0974769
 GENERAL INFORMATION:
 APPLICANT: THE BOARD OF TRUSTEES OF THE ILLINOIS CAMPBELL CENTER UNIVERSITY
 TITLE OF INVENTION: Patched Genes and their use
 NUMBER OF SEQUENCES: 19
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: P. de Bobbich, Test Administration & Control
 STREET: Four Embarcadero Center
 CITY: San Francisco
 STATE: CA
 COUNTRY: US
 ZIP: 94111
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Ver 01 #1.00
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: 05/0974769
 FILING DATE: 05-Oct-1997
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Rowland, Bertram I
 REGISTRATION NUMBER: 20015
 REFERENCE/DOCKET NUMBER: 460196
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-781-1989
 TELEFAX: 415-398-8249
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1285 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-059-13233-6

Query Match 47.5% Score: 48 DB: 3 Length: 1285
 Host Local Similarity: 58.3% Prod No: 460196
 Matches: 77 Conservative: 0 Mismatches: 51 Indels: 0

QY 3 HGTGCVLHPA 14

I I I I I I

DB 139 HDNNSVILHPA 150

REPORT 14
 1. NAME: [REDACTED]
 2. ADDRESS: [REDACTED]
 3. CITY: [REDACTED]
 4. STATE: [REDACTED]
 5. ZIP: [REDACTED]
 6. PHONE: [REDACTED]
 7. FAX: [REDACTED]
 8. E-MAIL: [REDACTED]
 9. OCCUPATION: [REDACTED]
 10. EDUCATION: [REDACTED]
 11. MARITAL STATUS: [REDACTED]
 12. NUMBER OF CHILDREN: [REDACTED]
 13. DATE OF BIRTH: [REDACTED]
 14. DATE OF DEATH: [REDACTED]
 15. DATE OF INTERVIEW: [REDACTED]
 16. DATE OF REPORT: [REDACTED]
 17. REPORTER: [REDACTED]
 18. REVIEWER: [REDACTED]
 19. APPROVER: [REDACTED]
 20. DISTRIBUTION: [REDACTED]

REPORT 14
 1. NAME: [REDACTED]
 2. ADDRESS: [REDACTED]
 3. CITY: [REDACTED]
 4. STATE: [REDACTED]
 5. ZIP: [REDACTED]
 6. PHONE: [REDACTED]
 7. FAX: [REDACTED]
 8. E-MAIL: [REDACTED]
 9. OCCUPATION: [REDACTED]
 10. EDUCATION: [REDACTED]
 11. MARITAL STATUS: [REDACTED]
 12. NUMBER OF CHILDREN: [REDACTED]
 13. DATE OF BIRTH: [REDACTED]
 14. DATE OF DEATH: [REDACTED]
 15. DATE OF INTERVIEW: [REDACTED]
 16. DATE OF REPORT: [REDACTED]
 17. REPORTER: [REDACTED]
 18. REVIEWER: [REDACTED]
 19. APPROVER: [REDACTED]
 20. DISTRIBUTION: [REDACTED]

REPORT 14
 1. NAME: [REDACTED]
 2. ADDRESS: [REDACTED]
 3. CITY: [REDACTED]
 4. STATE: [REDACTED]
 5. ZIP: [REDACTED]
 6. PHONE: [REDACTED]
 7. FAX: [REDACTED]
 8. E-MAIL: [REDACTED]
 9. OCCUPATION: [REDACTED]
 10. EDUCATION: [REDACTED]
 11. MARITAL STATUS: [REDACTED]
 12. NUMBER OF CHILDREN: [REDACTED]
 13. DATE OF BIRTH: [REDACTED]
 14. DATE OF DEATH: [REDACTED]
 15. DATE OF INTERVIEW: [REDACTED]
 16. DATE OF REPORT: [REDACTED]
 17. REPORTER: [REDACTED]
 18. REVIEWER: [REDACTED]
 19. APPROVER: [REDACTED]
 20. DISTRIBUTION: [REDACTED]

```

FEATURE:
LOCATION: 21
NAME/KEY: Xaa:Ser or Glu
FEATURE:
LOCATION: 58
NAME/KEY: Xaa:Arg or Met
FEATURE:
LOCATION: 59
NAME/KEY: Xaa:Val or Ala
FEATURE:
LOCATION: 61
NAME/KEY: Xaa:Glu or Glu
FEATURE:
LOCATION: 69
NAME/KEY: Xaa:Ala or Ser
FEATURE:
LOCATION: 77
NAME/KEY: Xaa:Tyr or Asp
US-08-451-409A-1

```

```

Query Match 46.28; Score 47; LB 1; Length 21;
Best Local Similarity 50.08; Pred. No. 6;
Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 1
QY 1 AEEGPTCWLHPPLA 14
IIII - - - -
DB 125 AEEGPTLIIINAVA 138

```

Search completed: August 22, 2001, 14:50:13
Job time: 364 sec



Nature 406, 959-964, 2000
 A>Title: Complete genome sequence of *Escherichia coli* strain FA1
 A:Reference number: AB29507
 A:Accession: M010:204337
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-417,510
 A:Cross-references: CH:AB009645; CH:AB009647; NID:49468259; PRI:06060303; GEN:06060303; GEN:06060303
 A:Experimental source: strain FA01
 C:Genetics:
 A:Gene: PA2115

Query Match 51.2% Score 417.00 Len 22 Length 4172
 Best Local Similarity 61.5% Pred. No. 107
 Matches 8: Conservative 1: Mismatches 4: Indels 0: Gaps 0

QY 1 ABGPTCWLHP. 13
 1 111111
 ID 295 ANVGECMLAPL 407

LT 14
 80
 Probable oxidoreductase PA5327 [Imported] *Streptococcus agalactiae* (strain FA1)
 C:Species: *Streptococcus agalactiae*
 C:Date: 15-Sep-2000 *Sequence Revision 15-Sep-2000* *RefSeq Project*
 C:Accession: AB29480
 C:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-442,510
 A:Cross-references: CH:AB009445; CH:AB009447; NID:49468259; PRI:06060303; GEN:06060303; GEN:06060303
 A:Experimental source: strain FA01
 C:Genetics:
 A:Gene: PA5327
 C:Superfamily: L-lactonolactone oxidase

Query Match 51.2% Score 417.00 Len 22 Length 4172
 Best Local Similarity 61.5% Pred. No. 107
 Matches 8: Conservative 1: Mismatches 4: Indels 0: Gaps 0

QY 1 ABGPTCWLHP. 13
 1 111111
 ID 295 ANVGECMLAPL 407

RESULT 15
 E86610
 axial filament protein [Imported] *Chlamydia pneumoniae* (strain J169)
 C:Species: *Chlamydia pneumoniae*
 C:Date: 02-Mar-2000 *Sequence Revision 02-Mar-2000* *RefSeq Project*
 C:Accession: E86610
 C:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-515,510
 A:Cross-references: CH:BA000008; NID:4877334; FID:BA000008; NID:4877334; NID:4877334
 A:Experimental source: strain J169
 C:Genetics:
 A:Gene: catE

Query Match 51.2% Score 417.00 Len 22 Length 4172
 Best Local Similarity 61.5% Pred. No. 107
 Matches 8: Conservative 1: Mismatches 4: Indels 0: Gaps 0

QY 2 ABGPTCWLHP. 13
 1 111111
 ID 453 ABGPTCWLHP. 407

Search completed: August 22, 2001, 14:21:44
 Job time: 78 sec

Wed Aug 22 15:42:59 2001

us-08-659-254-3.rpt

Page 6

PT lipid adrenal hyperplasia
 XX
 PS claim 1: pages 62-64; 89pp; English.
 XX
 CC The present sequence is the human *steroidogenesis acute regulatory protein* (hSTAR), conceptual lipid adrenal hyperplasia (LAP) associated mutation. Analysis of the hSTAR gene has revealed a mutation in the detected gene (provisional) of hAR associated with defects or a defect in the hAR gene. The hAR gene can be treated by protein or gene therapy, which can also be used to prevent or cure the transmission to children. hAR can be treated by protein or gene replacement therapy, which can also be used to prevent or cure the transmission to children.
 CC A human adrenal cortex cDNA library was screened with a mouse hAR probe to isolate a 1.6 kb insert, including an open reading frame. The residue protein. When it was cloned into a pSVcat and expressed in COS-1 cells cotransfected with pPRC-1, the hAR gene was used to level of progesterone synthesis in the presence of 17 α -OH progesterone.
 CC 20-alpha-hydroxyprogesterone.
 XX
 XX Sequence: 285 AA;
 SV
 Query Match: 100.0%; Pos: 1-17; Length: 285
 Local Similarity: 100.0%; Pos: 1-17; Length: 285
 Matches: 14; Conservative: 0; Mismatch: 0; Indels: 0; Pairs: 0
 YY 1 AERTCWLHRLA 14
 IIIIIIIIIIIIII
 DB 218 acbptcmhlp1a 241
 RESULT 8
 AAW13233
 ID AAW13233 standard; Protein, 285 AA.
 XX
 AC AAW13233;
 XX
 DT 21 MAY 1997 (first entry)
 DE Human steroidogenesis acute regulatory protein mutant (LAP) entry.
 XX
 DE Human steroidogenesis acute regulatory protein; hAR gene analysis; mutation detected; prenatal defects; acute adrenal hyperplasia; hAR gene; replacement therapy; hypercholesterolemia; mutation.
 KW
 KW lipid adrenal hyperplasia; treatment; steroidogenesis; protein replacement therapy; hypercholesterolemia; mutation.
 XX
 OS Homo sapiens.
 XX
 FE Key: Location/Qualifiers
 FI Miscellaneous: 169 /note "wild type gene located with 17"
 FT W09629438-A1.
 XX
 PD 26-SEP-1996.
 XX
 PF 22-MAR 1996; 96MO-0503896.
 XX
 PR 23-MAR 1995; 95DS-0410540.
 XX
 PA (RSC)) UNIV CALIFORNIA.
 PA (TYPE)) UNIV PENNSYLVANIA.
 XX
 PI Lin D, Miller ML, Strauss JF;
 XX
 DR WPI: 1996-44146/44.
 DR N-PSDB: AAT62019.
 XX
 PI Isolated human steroidogenesis acute regulatory protein gene used for detection of mutation(s) of this gene that cause congenital lipid adrenal hyperplasia
 XX
 PS claim 13: Page : 89pp; English.

CC The present sequence is the human *steroidogenesis acute regulatory protein* (hSTAR), conceptual lipid adrenal hyperplasia (LAP) associated mutation. Analysis of the hSTAR gene has revealed a mutation in the detected gene (provisional) of hAR associated with defects or a defect in the hAR gene. The hAR gene can be treated by protein or gene therapy, which can also be used to prevent or cure the transmission to children.
 CC A human adrenal cortex cDNA library was screened with a mouse hAR probe to isolate a 1.6 kb insert, including an open reading frame. The residue protein. When it was cloned into a pSVcat and expressed in COS-1 cells cotransfected with pPRC-1, the hAR gene was used to level of progesterone synthesis in the presence of 17 α -OH progesterone.
 CC 20-alpha-hydroxyprogesterone.
 XX
 XX Sequence: 285 AA;
 SV
 Query Match: 100.0%; Pos: 1-17; Length: 285
 Local Similarity: 100.0%; Pos: 1-17; Length: 285
 Matches: 14; Conservative: 0; Mismatch: 0; Indels: 0; Pairs: 0
 YY 1 AERTCWLHRLA 14
 IIIIIIIIIIIIII
 DB 218 acbptcmhlp1a 241
 RESULT 9
 AAW13233
 ID AAW13233 standard; Protein, 285 AA.
 XX
 AC AAW13233;
 XX
 DT 21 MAY 1997 (first entry)
 DE Human steroidogenesis acute regulatory protein mutant (LAP) entry.
 XX
 DE Human steroidogenesis acute regulatory protein; hAR gene analysis; mutation detected; prenatal defects; acute adrenal hyperplasia; hAR gene; replacement therapy; hypercholesterolemia; mutation.
 KW
 KW lipid adrenal hyperplasia; treatment; steroidogenesis; protein replacement therapy; hypercholesterolemia; mutation.
 XX
 OS Homo sapiens.
 XX
 FE Key: Location/Qualifiers
 FI Miscellaneous: 169 /note "wild type gene located with 17"
 FT W09629438-A1.
 XX
 PD 26-SEP-1996.
 XX
 PF 22-MAR 1996; 96MO-0503896.
 XX
 PR 23-MAR 1995; 95DS-0410540.
 XX
 PA (RSC)) UNIV CALIFORNIA.
 PA (TYPE)) UNIV PENNSYLVANIA.
 XX
 PI Lin D, Miller ML, Strauss JF;
 XX
 DR WPI: 1996-44146/44.
 DR N-PSDB: AAT62019.
 XX
 PI Isolated human steroidogenesis acute regulatory protein gene used for detection of mutation(s) of this gene that cause congenital lipid adrenal hyperplasia
 XX
 PS claim 13: Page : 89pp; English.
 XX
 PS Sequence: 285 AA;

Query Match 100.0% Score 400 28 22 Length 2953
 Best Local Similarity 100.0% Pred No. 19-152
 Matches 14 Conservative 0 Mismatches 0 Indels 0 Gaps 0

QY 1 AAFGTCWVLIHPLA 14
 | | | | | | | | | |
 DB 218 adpplcmvlihp1a 231

RESULT 12
 AAM13236
 ID AAM13246 standard: protein: 245 AA
 XX
 AC AAM13246
 XX

DI 21 MAY-1997 (first entry)
 XX

DE Human steroidogenesis acute regulatory protein (STAR) (MIM:261450)

XX Human steroidogenesis; acute regulatory protein (STAR) deficiency;
 mutation; detection; prenatal; genetic; directly; congenital; protein;
 lipid adrenal hyperplasia; treatment; replacement therapy;
 replacement therapy; hypercholesterolemia; mutant;
 XX

OS Homo sapiens.

PH Key Location/Qualifiers

PT Misc difference 218 /note: "wild type A a 3 defined with V1."

PN W06629338-A1

PD 26-SEP-1996

PF 22-MAR-1996; 96WD-0503896.

PK 23-MAR-1995; 95US-0410540.

PA (RRC) UNIV CALIFORNIA,
 (TYPE) UNIV PENNSYLVANIA.

PI Lin D, Miller W, Strauss JF

DR WPI: 1956-443130/44

DR N-PSDB; AAF62021

PT Isolated human steroidogenesis acute regulatory protein from a
 for detection of mutation(s) of this gene that cause congenital
 lipid adrenal hyperplasia

XX Claim 13: Page 1: 89pp; English.

XX The present sequence is the human steroidogenesis acute regulatory
 protein (STAR), congenital lipid adrenal hyperplasia (LAP)

XX associated mutant, A1218V. Analysis of the STAR gene for such a
 mutation is useful in the detection of congenital (1) of the

XX associated genetic defects, or its transmission to children. The
 can be treated by protein or gene replacement therapy, which can

XX also be used to prevent or treat type 1 diabetes mellitus.

XX Sequence 245 AA:

Query Match 95.0% Score 39 28 17 Length 2953

Best Local Similarity 100.0% Pred No. 19-152

Matches 14 Conservative 0 Mismatches 0 Indels 0 Gaps 0

QY 2 EHCPTCWLHPLA 14
 | | | | | | | | | |
 DB 219 ebplcmvlihp1a 241

RESULT 13

AAV72836
 ID AAV72846 standard: protein: 9 AA

XX AAV72846

DI 01 MAY-2001 (first entry)

DE Steroidogenesis acute regulatory protein (STAR) (MIM:261450)

XX Steroidogenesis; acute regulatory protein (STAR) deficiency;
 mutation; detection; prenatal; genetic; directly; congenital; protein;
 lipid adrenal hyperplasia; treatment; replacement therapy;
 replacement therapy; hypercholesterolemia; mutant;
 XX

XX Human steroidogenesis; acute regulatory protein (STAR) deficiency;
 mutation; detection; prenatal; genetic; directly; congenital; protein;
 lipid adrenal hyperplasia; treatment; replacement therapy;
 replacement therapy; hypercholesterolemia; mutant;
 XX

XX Human steroidogenesis; acute regulatory protein (STAR) deficiency;
 mutation; detection; prenatal; genetic; directly; congenital; protein;
 lipid adrenal hyperplasia; treatment; replacement therapy;
 replacement therapy; hypercholesterolemia; mutant;
 XX

OS Unidentifed.

PN US6194555-B1

PD 27 FEB 2001

PF 07 JUN 1996; 95US-0659254.

PK 04 NOV 1995; 95US-0538960.

PA (TYPE) UNIV HEALTH SCI CENT

PI Stereo DM, Clark MJ

DR WPI: 2001-21099722

PT Novel nucleotide encoding steroidogenesis acute regulatory protein
 useful for treating steroid hormone dependent disorders

XX Misosource: Column 12: 41pp; English

XX The invention relates to steroidogenesis acute regulatory protein
 (STAR) and nucleotide sequences encoding them. As proteins
 are used for regulating steroidogenesis, they are particularly the
 proteins are involved in regulation of steroidogenesis and
 the malfunctioning of a cell. The nucleotide sequences of the
 invention are useful in gene therapy for the treatment of steroid
 hormone-dependent disorders, particularly lipid congenital
 adrenal hyperplasia (LAP), intersex, 21-hydroxylase deficiency,
 androgen-responsive tumours, precocious puberty, Klinefelter
 syndrome, adrenal hyperplasia congenita, and adrenoleukodystrophy
 hypoadrenalism. They are also useful for treatment of
 the steroidogenesis acute regulatory protein

XX The present sequence is steroidogenesis acute regulatory protein (STAR)
 peptide. This peptide is useful for treatment of adrenoleukodystrophy
 screening and identifying and large deletions of STAR protein.

XX Sequence 9 AA:

Query Match 66.2% Score 39 18 17 Length 2953

Best Local Similarity 100.0% Pred No. 19-152

Matches 9 Conservative 0 Mismatches 0 Indels 0 Gaps 0

QY 1 AAFGTCWVLIHPLA 14
 | | | | | | | | | |
 DB 1 adpplcmvlihp1a 231

AAV72836
 ID AAV72846 standard: protein: 9 AA

XX AAV72846

DI 01 MAY-2001 (first entry)

DE Steroidogenesis acute regulatory protein (STAR) (MIM:261450)

XX Steroidogenesis; acute regulatory protein (STAR) deficiency;
 mutation; detection; prenatal; genetic; directly; congenital; protein;
 lipid adrenal hyperplasia; treatment; replacement therapy;
 replacement therapy; hypercholesterolemia; mutant;
 XX

XX Human steroidogenesis; acute regulatory protein (STAR) deficiency;
 mutation; detection; prenatal; genetic; directly; congenital; protein;
 lipid adrenal hyperplasia; treatment; replacement therapy;
 replacement therapy; hypercholesterolemia; mutant;
 XX

XX Human steroidogenesis; acute regulatory protein (STAR) deficiency;
 mutation; detection; prenatal; genetic; directly; congenital; protein;
 lipid adrenal hyperplasia; treatment; replacement therapy;
 replacement therapy; hypercholesterolemia; mutant;
 XX

OS Unidentifed.

PN US6194555-B1

PD 27 FEB 2001

PF 07 JUN 1996; 95US-0659254.

PK 04 NOV 1995; 95US-0538960.

PA (TYPE) UNIV HEALTH SCI CENT

PI Stereo DM, Clark MJ

DR WPI: 2001-21099722

PT Novel nucleotide encoding steroidogenesis acute regulatory protein
 useful for treating steroid hormone dependent disorders

XX Misosource: Column 12: 41pp; English

XX The invention relates to steroidogenesis acute regulatory protein
 (STAR) and nucleotide sequences encoding them. As proteins
 are used for regulating steroidogenesis, they are particularly the
 proteins are involved in regulation of steroidogenesis and
 the malfunctioning of a cell. The nucleotide sequences of the
 invention are useful in gene therapy for the treatment of steroid
 hormone-dependent disorders, particularly lipid congenital
 adrenal hyperplasia (LAP), intersex, 21-hydroxylase deficiency,
 androgen-responsive tumours, precocious puberty, Klinefelter
 syndrome, adrenal hyperplasia congenita, and adrenoleukodystrophy
 hypoadrenalism. They are also useful for treatment of
 the steroidogenesis acute regulatory protein

XX The present sequence is steroidogenesis acute regulatory protein (STAR)
 peptide. This peptide is useful for treatment of adrenoleukodystrophy
 screening and identifying and large deletions of STAR protein.

XX Sequence 9 AA:

Z

[illegible]

W

100
 90
 80
 70
 60
 50
 40
 30
 20
 10
 0

—

History of the Church

www.villaworld.com

100

1. *Chlorophyll a* and *Chlorophyll b* contents were determined by spectrophotometry using the method of Lichtenthaler and Whistler (1973).

[illegible]

1. *Phragmites* (Common Reed)

Phosphorylation of casein

100

Form of a letter

1000

1. The first group of symbols is the set of natural numbers \mathbb{N} .

[illegible]

—

—

— — — — —

Appendix

Index

2. $\lim_{n \rightarrow \infty} \frac{1}{n} \sum_{k=1}^n \frac{1}{k} = 0$

Figure 1 is a schematic representation of the experimental design. It shows a flow from 'STIMULI' to 'RESPONSE' and 'PERFORMANCE'. 'STIMULI' includes 'Visual' and 'Auditory'. 'RESPONSE' includes 'Correct' and 'Incorrect'. 'PERFORMANCE' includes 'Accuracy' and 'Reaction Time'. The flow is indicated by arrows.

1000

1



187. 188. 189. 190. 191. 192. 193. 194. 195. 196. 197. 198. 199. 200. 201. 202. 203. 204. 205. 206. 207. 208. 209. 210. 211. 212. 213. 214. 215. 216. 217. 218. 219. 220. 221. 222. 223. 224. 225. 226. 227. 228. 229. 230. 231. 232. 233. 234. 235. 236. 237. 238. 239. 240. 241. 242. 243. 244. 245. 246. 247. 248. 249. 250. 251. 252. 253. 254. 255. 256. 257. 258. 259. 260. 261. 262. 263. 264. 265. 266. 267. 268. 269. 270. 271. 272. 273. 274. 275. 276. 277. 278. 279. 280. 281. 282. 283. 284. 285. 286. 287. 288. 289. 290. 291. 292. 293. 294. 295. 296. 297. 298. 299. 300. 301. 302. 303. 304. 305. 306. 307. 308. 309. 310. 311. 312. 313. 314. 315. 316. 317. 318. 319. 320. 321. 322. 323. 324. 325. 326. 327. 328. 329. 330. 331. 332. 333. 334. 335. 336. 337. 338. 339. 340. 341. 342. 343. 344. 345. 346. 347. 348. 349. 350. 351. 352. 353. 354. 355. 356. 357. 358. 359. 360. 361. 362. 363. 364. 365. 366. 367. 368. 369. 370. 371. 372. 373. 374. 375. 376. 377. 378. 379. 380. 381. 382. 383. 384. 385. 386. 387. 388. 389. 390. 391. 392. 393. 394. 395. 396. 397. 398. 399. 400. 401. 402. 403. 404. 405. 406. 407. 408. 409. 410. 411. 412. 413. 414. 415. 416. 417. 418. 419. 420. 421. 422. 423. 424. 425. 426. 427. 428. 429. 430. 431. 432. 433. 434. 435. 436. 437. 438. 439. 440. 441. 442. 443. 444. 445. 446. 447. 448. 449. 450. 451. 452. 453. 454. 455. 456. 457. 458. 459. 460. 461. 462. 463. 464. 465. 466. 467. 468. 469. 470. 471. 472. 473. 474. 475. 476. 477. 478. 479. 480. 481. 482. 483. 484. 485. 486. 487. 488. 489. 490. 491. 492. 493. 494. 495. 496. 497. 498. 499. 500. 501. 502. 503. 504. 505. 506. 507. 508. 509. 510. 511. 512. 513. 514. 515. 516. 517. 518. 519. 520. 521. 522. 523. 524. 525. 526. 527. 528. 529. 530. 531. 532. 533. 534. 535. 536. 537. 538. 539. 540. 541. 542. 543. 544. 545. 546. 547. 548. 549. 550. 551. 552. 553. 554. 555. 556. 557. 558. 559. 560. 561. 562. 563. 564. 565. 566. 567. 568. 569. 570. 571. 572. 573. 574. 575. 576. 577. 578. 579. 580. 581. 582. 583. 584. 585. 586. 587. 588. 589. 590. 591. 592. 593. 594. 595. 596. 597. 598. 599. 600. 601. 602. 603. 604. 605. 606. 607. 608. 609. 610. 611. 612. 613. 614. 615. 616. 617. 618. 619. 620. 621. 622. 623. 624. 625. 626. 627. 628. 629. 630. 631. 632. 633. 634. 635. 636. 637. 638. 639. 640. 641. 642. 643. 644. 645. 646. 647. 648. 649. 650. 651. 652. 653. 654. 655. 656. 657. 658. 659. 660. 661. 662. 663. 664. 665. 666. 667. 668. 669. 670. 671. 672. 673. 674. 675. 676. 677. 678. 679. 680. 681. 682. 683. 684. 685. 686. 687. 688. 689. 690. 691. 692. 693. 694. 695. 696. 697. 698. 699. 700. 701. 702. 703. 704. 705. 706. 707. 708. 709. 710. 711. 712. 713. 714. 715. 716. 717. 718. 719. 720. 721. 722. 723. 724. 725. 726. 727. 728. 729. 730. 731. 732. 733. 734. 735. 736. 737. 738. 739. 740. 741. 742. 743. 744. 745. 746. 747. 748. 749. 750. 751. 752. 753. 754. 755. 756. 757. 758. 759. 760. 761. 762. 763. 764. 765. 766. 767. 768. 769. 770. 771. 772. 773. 774. 775. 776. 777. 778. 779. 780. 781. 782. 783. 784. 785. 786. 787. 788. 789. 790. 791. 792. 793. 794. 795. 796. 797. 798. 799. 800. 801. 802. 803. 804. 805. 806. 807. 808. 809. 810. 811. 812. 813. 814. 815. 816. 817. 818. 819. 820. 821. 822. 823. 824. 825. 826. 827. 828. 829. 830. 831. 832. 833. 834. 835. 836. 837. 838. 839. 840. 841. 842. 843. 844. 845. 846. 847. 848. 849. 850. 851. 852. 853. 854. 855. 856. 857. 858. 859. 860. 861. 862. 863. 864. 865. 866. 867. 868. 869. 870. 871. 872. 873. 874. 875. 876. 877. 878. 879. 880. 881. 882. 883. 884. 885. 886. 887. 888. 889. 890. 891. 892. 893. 894. 895. 896. 897. 898. 899. 900. 901. 902. 903. 904. 905. 906. 907. 908. 909. 910. 911. 912. 913. 914. 915. 916. 917. 918. 919. 920. 921. 922. 923. 924. 925. 926. 927. 928. 929. 930. 931. 932. 933. 934. 935. 936. 937. 938. 939. 940. 941. 942. 943. 944. 945. 946. 947. 948. 949. 950. 951. 952. 953. 954. 955. 956. 957. 958. 959. 960. 961. 962. 963. 964. 965. 966. 967. 968. 969. 970. 971. 972. 973. 974. 975. 976. 977. 978. 979. 980. 981. 982. 983. 984. 985. 986. 987. 988. 989. 990. 991. 992. 993. 994. 995. 996. 997. 998. 999. 1000.

Wed Aug 22 15:42:58 2001

us-08-659-254-18.rsp

Page 10

10. EMPLOYER: ALEXANDER, JAMES
11. HUSBAND: JAMES ALEXANDER
12. SPOUSE: JAMES ALEXANDER

13. SOURCE: MARY ANN
14. SOURCE: MARY ANN
15. SOURCE: MARY ANN

16. SOURCE: MARY ANN
17. SOURCE: MARY ANN
18. SOURCE: MARY ANN

19. SOURCE: MARY ANN
20. SOURCE: MARY ANN
21. SOURCE: MARY ANN

22. SOURCE: MARY ANN
23. SOURCE: MARY ANN
24. SOURCE: MARY ANN

25. SOURCE: MARY ANN
26. SOURCE: MARY ANN
27. SOURCE: MARY ANN

28. SOURCE: MARY ANN
29. SOURCE: MARY ANN
30. SOURCE: MARY ANN

31. SOURCE: MARY ANN
32. SOURCE: MARY ANN
33. SOURCE: MARY ANN

34. SOURCE: MARY ANN
35. SOURCE: MARY ANN
36. SOURCE: MARY ANN

37. SOURCE: MARY ANN
38. SOURCE: MARY ANN
39. SOURCE: MARY ANN

40. SOURCE: MARY ANN
41. SOURCE: MARY ANN
42. SOURCE: MARY ANN

43. SOURCE: MARY ANN
44. SOURCE: MARY ANN
45. SOURCE: MARY ANN

46. SOURCE: MARY ANN
47. SOURCE: MARY ANN
48. SOURCE: MARY ANN

49. SOURCE: MARY ANN
50. SOURCE: MARY ANN
51. SOURCE: MARY ANN

52. SOURCE: MARY ANN
53. SOURCE: MARY ANN
54. SOURCE: MARY ANN

55. SOURCE: MARY ANN
56. SOURCE: MARY ANN
57. SOURCE: MARY ANN

58. SOURCE: MARY ANN
59. SOURCE: MARY ANN
60. SOURCE: MARY ANN

61. SOURCE: MARY ANN
62. SOURCE: MARY ANN
63. SOURCE: MARY ANN

64. SOURCE: MARY ANN
65. SOURCE: MARY ANN
66. SOURCE: MARY ANN

67. SOURCE: MARY ANN
68. SOURCE: MARY ANN
69. SOURCE: MARY ANN

70. SOURCE: MARY ANN
71. SOURCE: MARY ANN
72. SOURCE: MARY ANN

73. SOURCE: MARY ANN
74. SOURCE: MARY ANN
75. SOURCE: MARY ANN

76. SOURCE: MARY ANN
77. SOURCE: MARY ANN
78. SOURCE: MARY ANN

79. SOURCE: MARY ANN
80. SOURCE: MARY ANN
81. SOURCE: MARY ANN

82. SOURCE: MARY ANN
83. SOURCE: MARY ANN
84. SOURCE: MARY ANN

85. SOURCE: MARY ANN
86. SOURCE: MARY ANN
87. SOURCE: MARY ANN

88. SOURCE: MARY ANN
89. SOURCE: MARY ANN
90. SOURCE: MARY ANN

91. SOURCE: MARY ANN
92. SOURCE: MARY ANN
93. SOURCE: MARY ANN

94. SOURCE: MARY ANN
95. SOURCE: MARY ANN
96. SOURCE: MARY ANN

97. SOURCE: MARY ANN
98. SOURCE: MARY ANN
99. SOURCE: MARY ANN

100. SOURCE: MARY ANN
101. SOURCE: MARY ANN
102. SOURCE: MARY ANN

103. SOURCE: MARY ANN
104. SOURCE: MARY ANN
105. SOURCE: MARY ANN

106. SOURCE: MARY ANN
107. SOURCE: MARY ANN
108. SOURCE: MARY ANN

109. SOURCE: MARY ANN
110. SOURCE: MARY ANN
111. SOURCE: MARY ANN

112. SOURCE: MARY ANN
113. SOURCE: MARY ANN
114. SOURCE: MARY ANN

115. SOURCE: MARY ANN
116. SOURCE: MARY ANN
117. SOURCE: MARY ANN

Page 7



GenCore version 4.5
Copyright (c) 1994 - 2000 Computer Link

OM protein - protein search, using sw method

Run on: August 22, 2001, 14:30:17

(Execution time: 0:05)
(66,136 Million cell updates/sec)

Title: US-08-659-254-18

Perfect score: 1470

Sequence: 1 MLLATPEKLNCSYHBMNM

Scoring table:

Matrix: BLOSUM62

Gapop: 10.0, Gapext: 0.5

Searched: 197345 seqs, 2059046 residues

Total number of hits satisfying chosen parameters: 10739

Minimum DB seq length: 0

Minimum DB seq length: 200000000

Post-processing: Minimum Match: 0%

Maximum Match: 100%

Listing first 45 summaries

Database: Issued_Patents_AA*

Result No. is the number of results produced by above parameters
score greater than or equal to the score of the result being printed
and is defined by analysis of the hit score threshold.

SUMMARY

| Result No. | Score | Query Match | Length | DB | ID | Description |
|------------|--------|-------------|--------|----|------------------|--------------------------------------|
| 1 | 1470 | 100.0 | 285 | 4 | US-08-659-254-18 | Sequence 18, Application US/08659254 |
| 2 | 1464 | 99.6 | 285 | 1 | US-08-659-254-18 | Sequence 18, Application US/08659254 |
| 3 | 1291.5 | 87.9 | 284 | 2 | US-08-659-254-18 | Sequence 18, Application US/08659254 |
| 4 | 1258.5 | 85.6 | 276 | 4 | US-08-659-254-18 | Sequence 18, Application US/08659254 |
| 5 | 372 | 25.3 | 115 | 2 | US-08-659-254-18 | Sequence 18, Application US/08659254 |
| 6 | 104 | 7.1 | 988 | 2 | US-08-659-254-18 | Sequence 18, Application US/08659254 |
| 7 | 104 | 7.1 | 988 | 2 | US-08-659-254-18 | Sequence 18, Application US/08659254 |
| 8 | 98.5 | 6.7 | 291 | 4 | US-08-659-254-18 | Sequence 18, Application US/08659254 |
| 9 | 90.5 | 6.2 | 494 | 4 | US-08-659-254-18 | Sequence 18, Application US/08659254 |
| 10 | 89 | 6.1 | 19 | 2 | US-08-659-254-18 | Sequence 18, Application US/08659254 |
| 11 | 85 | 6.1 | 19 | 4 | US-08-659-254-18 | Sequence 18, Application US/08659254 |
| 12 | 83 | 5.6 | 402 | 4 | US-08-659-254-18 | Sequence 18, Application US/08659254 |
| 13 | 82 | 5.6 | 402 | 4 | US-08-659-254-18 | Sequence 18, Application US/08659254 |
| 14 | 82 | 5.6 | 600 | 5 | US-08-659-254-18 | Sequence 18, Application US/08659254 |
| 15 | 81 | 5.5 | 529 | 4 | US-08-659-254-18 | Sequence 18, Application US/08659254 |
| 16 | 81 | 5.5 | 529 | 4 | US-08-659-254-18 | Sequence 18, Application US/08659254 |
| 17 | 80 | 5.4 | 14 | 2 | US-08-659-254-18 | Sequence 18, Application US/08659254 |
| 18 | 80 | 5.4 | 14 | 4 | US-08-659-254-18 | Sequence 18, Application US/08659254 |
| 19 | 79.5 | 5.4 | 942 | 4 | US-08-659-254-18 | Sequence 18, Application US/08659254 |
| 20 | 79.5 | 5.4 | 942 | 4 | US-08-659-254-18 | Sequence 18, Application US/08659254 |
| 21 | 79 | 5.4 | 942 | 4 | US-08-659-254-18 | Sequence 18, Application US/08659254 |
| 22 | 78.5 | 5.3 | 786 | 4 | US-08-659-254-18 | Sequence 18, Application US/08659254 |
| 23 | 77.5 | 5.3 | 255 | 1 | US-08-659-254-18 | Sequence 18, Application US/08659254 |
| 24 | 77.5 | 5.3 | 255 | 1 | US-08-659-254-18 | Sequence 18, Application US/08659254 |
| 25 | 77.5 | 5.3 | 572 | 4 | US-08-659-254-18 | Sequence 18, Application US/08659254 |
| 26 | 77.5 | 5.3 | 572 | 4 | US-08-659-254-18 | Sequence 18, Application US/08659254 |
| 27 | 76.5 | 5.2 | 222 | 2 | US-08-659-254-18 | Sequence 18, Application US/08659254 |

28 76.5 5.2 222 4 US-08-659-254-18
29 76.5 5.2 222 4 US-08-659-254-18
30 76.5 5.2 222 4 US-08-659-254-18
31 76 5.2 222 4 US-08-659-254-18
32 76 5.2 222 4 US-08-659-254-18
33 76 5.2 222 4 US-08-659-254-18
34 75 5.1 145 2 US-08-659-254-18
35 75 5.1 145 2 US-08-659-254-18
36 74.5 5.1 793 4 US-08-659-254-18
37 74 5.0 699 4 US-08-659-254-18
38 74 5.0 699 4 US-08-659-254-18
39 74 5.0 719 4 US-08-659-254-18
40 74 5.0 719 4 US-08-659-254-18
41 73 5.0 719 4 US-08-659-254-18
42 74 5.0 740 4 US-08-659-254-18
43 74 5.0 740 4 US-08-659-254-18
44 74 5.0 740 4 US-08-659-254-18
45 74 5.0 740 4 US-08-659-254-18

ALL HITS

RESULT 1
US-08-659-254-18
Sequence 18, Application US/08659254
Patent No. 6194156
GENERAL INFORMATION
APPLICANT: STORCO, Douglas M.
APPLICANT: STORCO, Douglas M.
ATTORNEY: STORCO, Douglas M.
TITLE: 78701
COMPUTER REVENUE FORM
MEDIUM TYPE: floppy disk
OPERATING SYSTEM: pc-compatible
SOFTWARE: Patent In Release #1.0, Version #1.0
CURRENT APPLICATION DATA
ATTORNEY: STORCO, Douglas M.
FILING DATE: 07 JUN 1996
CLASSIFICATION: 5.00
PRIOR APPLICATION DATA
ATTORNEY: STORCO, Douglas M.
FILING DATE: 04 OCT 1995
ATTORNEY: STORCO, Douglas M.
NAME: MAYFIELD, Douglas L.
REGISTRATION NUMBER: 44772
REFERENCE/OTHER NUMBERS: 44772, 44772
TELEPHONE: 1-740-762-0000
TELEFAX: 1-740-762-0000
INFORMATION FOR SEQ ID NO: 18
SEQUENCE CHARACTERISTICS
LENGTH: 285 amino acids
TYPE: amino acid
TOPOLOGY: 110000
US-08-659-254-18

Query Match: 100.0% Score: 1470
Best Local Similarity: 100.0% P-Value: 1.0e-54
Database: 2059046 seqs, 2059046 residues
1 MLLATPEKLNCSYHBMNM

Aug 22 15:42:57 2001

us-08-659-254-18.rail

07 181 PEEVSVCAAPRSTVLAAMATDEONMREK V IASBETONVHIFACSESKIT 240
180 PEEVSVCAAPRSTVLAAMATDEONMREK V IASBETONVHIFACSESKIT 240
07 241 WLSLDEKGM PKSTINNOV SOTODFANIKKLSHPASERD 285
240 WLSLDEKGM PKSTINNOV SOTODFANIKKLSHPASERD 285

RESULT 4
US-08-659-254-2
Sequence 2, Application US/08659254
Patent No. 6194555

GENERAL INFORMATION:
APPLICANT: Stocco, Douglas M.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR REGULATION

NUMBER OF INVENTION: OF STEROIDOTENEIS
NUMBER OF SEQUENCES: 19

CORRESPONDENCE ADDRESS:
ADDRESSEE: Akio, Gump, Strauss, Hauer & Field, L.L.P.
STREET: 1900 Frost Bank Plaza, 810 Redress Avenue
CITY: Austin
STATE: TX

COUNTRY: U.S.A.
ZIP: 78701

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #11, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/659, 254
FILING DATE: 07-JUN-1996

CLASSIFICATION 530
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/538, 360
FILING DATE: 04-OCT-1995

ATTORNEY/AGENT INFORMATION:
NAME: Mayfield, Denise L.
REGISTRATION NUMBER: 33,732
REFERENCE/DOCKET NUMBER: 43375-0006

TELEPHONE: 512/499-6290
TELEFAX: 512/499-6290

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 276 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: protein
US-08-659-254-2

Query Match 85.0% Score 107.57 DB 4 Length 276
Best Local Similarity 97.4% Pos 1 Pos 2 Pos 3 Pos 4 Pos 5
Matches 242, Conservative 18, Mismatches 16, Indels 4, Gaps 1

07 1 MLATFKLCASSYRHHNNKGLPQAVATGELNRALGDTPTV NVWERSSTL 40
1 MLATFKLCASSYRHHNNKGLPQAVATGELNRALGDTPTV NVWERSSTL 40

07 1 MLATFKLCASSYRHHNNKGLPQAVATGELNRALGDTPTV NVWERSSTL 40
1 MLATFKLCASSYRHHNNKGLPQAVATGELNRALGDTPTV NVWERSSTL 40

07 61 SLEPELVSDJAVIQQGEFAMKAT 3156 KKKKFFSGGGRN KAVGVYH 470
61 SLEPELVSDJAVIQQGEFAMKAT 3156 KKKKFFSGGGRN KAVGVYH 470

07 121 RLEVVDPMPKATVYERHFMKGVNREK 4500 KKKKFFSGGGRN KAVGVYH 470
121 RLEVVDPMPKATVYERHFMKGVNREK 4500 KKKKFFSGGGRN KAVGVYH 470

07 181 PRQVSVRCARRGSTVLAAMATDEONMREK V IASBETONVHIFACSESKIT 240
181 PRQVSVRCARRGSTVLAAMATDEONMREK V IASBETONVHIFACSESKIT 240

DB 180 PEEVSVCAAPRSTVLAAMATDEONMREK V IASBETONVHIFACSESKIT 240
180 PEEVSVCAAPRSTVLAAMATDEONMREK V IASBETONVHIFACSESKIT 240
07 241 WLSLDEKGM PKSTINNOV SOTODFANIKKLSHPASERD 285
240 WLSLDEKGM PKSTINNOV SOTODFANIKKLSHPASERD 285

RESULT 5
US-08-691-814B-6
Sequence 6, Application US/08691814B
Patent No. 5981218

GENERAL INFORMATION:
APPLICANT: Kuo, Marie-Christine
TITLE OF INVENTION: Isolated Nucleic Acid Molecule and a Breast Cancer Protein

NUMBER OF INVENTION: 124
NUMBER OF SEQUENCES: 124

CORRESPONDENCE ADDRESS:
ADDRESSEE: Shure, Kessler, Colston & Fox P.C.
STREET: 1100 New York Ave, NW, Suite 400
CITY: Washington
STATE: DC

COUNTRY: USA
ZIP: 20005-3314

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #11, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/691, 814B
FILING DATE: 01-JUN-1996

CLASSIFICATION 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 60/207, 288
FILING DATE: 09-AUG-1995

ATTORNEY/AGENT INFORMATION:
NAME: Stocco, Denise L.
REGISTRATION NUMBER: 36,588
REFERENCE/DOCKET NUMBER: 181, 000, 911

TELEPHONE: 202-371-2600
TELEFAX: 202-371-2600

INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 445 amino acids
TYPE: amino acid
STRANDEDNESS: linear
TOPOLOGY: linear

MOLECULE TYPE: protein
US-08-691-814B-6

Query Match 25.38% Score 172.08 DB 2 Length 445
Best Local Similarity 47.5% Pos 1 Pos 2 Pos 3 Pos 4 Pos 5
Matches 78, Conservative 45, Mismatches 85, Indels 2, Gaps 1

07 68 VSLDVLAVQGHKAMKALDLSNVA 2156 KKKKFFSGGGRN KAVGVYH 470
68 VSLDVLAVQGHKAMKALDLSNVA 2156 KKKKFFSGGGRN KAVGVYH 470

07 128 QVHRIYELVVRHFMKGVNREK 4500 KKKKFFSGGGRN KAVGVYH 470
128 QVHRIYELVVRHFMKGVNREK 4500 KKKKFFSGGGRN KAVGVYH 470

07 241 RLEVVDPMPKATVYERHFMKGVNREK 4500 KKKKFFSGGGRN KAVGVYH 470
241 RLEVVDPMPKATVYERHFMKGVNREK 4500 KKKKFFSGGGRN KAVGVYH 470

07 451 RLEVVDPMPKATVYERHFMKGVNREK 4500 KKKKFFSGGGRN KAVGVYH 470
451 RLEVVDPMPKATVYERHFMKGVNREK 4500 KKKKFFSGGGRN KAVGVYH 470

07 240 WLSLDEKGM PKSTINNOV SOTODFANIKKLSHPASERD 285
240 WLSLDEKGM PKSTINNOV SOTODFANIKKLSHPASERD 285

LENGTH: 988 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-980 357-19

Query Match 7.1% Score 104 R 4 Length 988
 Best Local Similarity 20.7% Ident. No. 21
 Matches 58 Conservative 50 Mismatches 80 Gaps 12

41 GGTSTNNVPR-----
 221 GHPSTPTKTFPLPYTRGMDIETVQISLPSALSTLSGSPVQVADNKKRRT 292
 73 ---LAVLQGEFAMOKA -----LQTLNGLNKKSTGSGVAVGKQV EYV 316
 281 STLTITLDTLFDLIDKAEIHDROTLSTSKNKGDLTKGPKVYVQVQVQVQV 409
 119 VRLKVVVQVPMRLDYERVENMEACMPCV 174 274 GGGGGG 447 574
 340 ---QALLKAREKL--DVEKVLDSYLVN- ----LVS--SVFADEL 474
 179 VGRDFVSVGCAFKESTVAFARATFSNKK 214 244 GGGGGG 474
 376 ARPADY-----DYLDELKRTYSLKRTPT FLSGLTDS EAN 414
 219 LITLSTLIDKEMLPSTINGVIGOTOVLANHKELESE 278
 414 SPILQAVFLLPNNKSGPKVPPVQVQVQVQVQVQVQVQVQVQVQVQVQV 450

RESULT 8
 US-09-328-869-2
 Sequence 2, Application US/0932869
 Patent No. 616863
 GENERAL INFORMATION:
 APPLICANT: Kaser, Matthew, R.
 APPLICANT: Hillman, Jennifer, R.
 APPLICANT: Roubin, Mariah, R.
 TITLE OF INVENTION: PROSTHOLIPID TRANSFER PROTEIN
 FILE REFERENCE: PC-0003 US
 CURRENT APPLICATION NUMBER: US/09/328 869-2
 CURRENT FILING DATE: 1999-06-08
 NUMBER OF SEQ ID NOS: 17
 SOFTWARE: PERL Program
 SEQ ID NO: 2
 LENGTH: 291
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE:
 OTHER INFORMATION: 1772859CD)
 US-09-328-869-2

Query Match 6.7% Score 94.5 R 4 Length 291
 Best Local Similarity 23.8% Ident. No. 1012
 Matches 34 Conservative 26 Mismatches 56 Gaps 27 Gaps 4

127 DCHRELYELVENMEACMPCV 174 274 GGGGGG 447 574
 76 DWAEELIYDLD-TEYRKMDSYH-----EEDADLTVNADAVTNRQ 124
 181 ---PDDVSVRCARQSTCYLAGM DLEIMHCKVIAHNGPQVNIHQ ANSES 258
 122 FRTLKHVITLPSM PMNAVYTHNV VZVGVVQVQVQVQVQVQVQVQVQV 174
 239 KIVATVITSLKGM PKSLIN 258
 186 SCVITVLAQVPHQSTFKWVKE 202

RESULT 9

US-09-198-956-2
 Sequence 2, Application US/09198956
 Patent No. 6165769
 GENERAL INFORMATION:
 APPLICANT: Anderson, Leon N.
 APPLICANT: Scholten, Martin
 APPLICANT: Lohse, Heide Erik K.
 APPLICANT: Biernat, Mads B.
 APPLICANT: Schmitz, Kirk
 TITLE OF INVENTION: Method for Regulating the Growth of Cells
 FILE REFERENCE: 5377,200-US
 CURRENT FILING DATE: 1998-11-24
 CURRENT FILING DATE: 1998-11-24
 EARLIER FILING DATE: 1997-11-24
 EARLIER FILING DATE: 1997-11-24
 NUMBER OF SEQ ID NOS: 26
 SOFTWARE: FastSeq 1.0 Windows Version 1.0
 SEQ ID NO: 2
 LENGTH: 494
 TYPE: PRT
 ORGANISM: Bacul. Tus. licheniformis
 US-09-198-956-2

Query Match 6.2% Score 90.5 R 4 Length 494
 Best Local Similarity 22.8% Ident. No. 1012
 Matches 59 Conservative 39 Mismatches 119 Gaps 10

52 VRRSSDLSKDELTATGATGDE 174 274 GGGGGG 447 574
 40 LKESL--SDNITFANCPHATKAKV 174 274 GGGGGG 447 574
 112 VVTVVQVPMRLDYERVENMEACMPCV 174 274 GGGGGG 447 574
 90 ---DSKLIHDAVLSNNVAVVYD 174 274 GGGGGG 447 574
 159 ELAEANMLVPRVSVK 174 274 GGGGGG 447 574
 138 KIVASARGLAELASCVLAKK 174 274 GGGGGG 447 574
 166 FANMATVNMPOKQVIAHNGPQVNIHQ ANSES 258
 198 LKRVVAVVQVPMRLDYERVENMEACMPCV 174 274 GGGGGG 447 574
 259 VLSQVDFANHKKRL 281
 257 YPRFASGVNFKRNTADNS 281

RESULT 10
 US-08-548-960-5
 Sequence 5, Application US/08548960
 Patent No. 5872240
 GENERAL INFORMATION:
 APPLICANT: Stocco, Douglas M.
 APPLICANT: Clark, Barbara J.
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
 NUMBER OF SEQUENCES: 14
 CORRESPONDING ADDRESS:
 ADDRESS: Attn. Gump, Suzanne, 6000 E. 1st Ave.,
 Street: 1900 First Bank Plaza, Box 60000, Denver, CO 80202
 CITY: Austin
 STATE: TX
 COUNTRY: U.S.A.
 ZIP: 78701
 COMPUTER READABLE FORM:
 MEDIA TYPE: ASCII disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC DOS/MS-DOS

Aug 22 15:42:57 2001

us-08-659-254-18.ra1

Page 7

QY 270 HUKR 274
DB 260 EKEFAI-----TFKATCNIJH-----TFPMVNVNLEHPSWSPFAU 294

QY 270 HUKR 274
DB 295 RI000 299

RESULT 13
US-09 414-664-4
Sequence 4, Application US/09414664
Patent No. 6242249

GENERAL INFORMATION:
APPLICANT: Lawlor, Elizabeth J.
TITLE OF INVENTION: No. 6242249el file
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESS: Dechert Price & Rhoads
STREET: 4000 Bell Atlantic Tower, 11th Arch St.
CITY: Philadelphia
STATE: PA
COUNTRY: US
ZIP: 19103

COMPUTER READABLE FORM:
MEDIUM TYPE: diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: DOS Windows Vars. 1.2.0

SOFTWARE: FASTSP for Windows Vars. 1.2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09414,664
FILING DATE:

CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 09/999,339
FILING DATE:

ATTORNEY/AGENT INFORMATION:
NAME: Falk, Stephen T.
REGISTRATION NUMBER: 36,795
REFERENCE/AGENT NUMBER: 0810045
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-994-2488
TELEFAX: 215-994-2222

TELEX:
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 402 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

09-414-664-4

Query Match 5.68; Score 41; FR 4; Length 402;
Best Local Similarity 23.38; Pctid No. 4;
Matches 57; Conservative 37; Missed 71; Gaps 11;

QY 64 EETLYGGLAVYGGFFAMAKATLLHGTAPFVGGQNGGVSWSVAVAKV 120
DB 101 QETLSIDRL-----GEALDHSIGHLAEVYVNDVVERVQDVIYVQPSVWQPPPPG 154
QY 121 -----KLVVIAHREELIEEYVMRYGNNMNN 150
DB 154 QDAECYELFTGSGSPFPGFFEQLEKMKVDFKLVVTFLETHADRIAEKVA-----EKIK 210
QY 151 VETIVVIGKPTPTFTTHAEADNANVTPEVSVVAKVNSVIVATMAVHNM 279
DB 211 VAEITFEVDFCTPTTAHLEFAEAHYVPEVQHPQVNSK-----ADKAVNV 259
QY 210 PRKGVVTRRRRTGMVJHPLASPSKLTLLGELIKVAVETKQVDSQVNVGN 299
DB 260 EKEFAI-----TKADNLTID-----PLAVNLEHPSWSPFAU 294

QY 270 HUKR 274
DB 295 RI000 299

RESULT 14
PCT-US95-10166-2
Sequence 2, Application PCT/US9510166
GENERAL INFORMATION:

APPLICANT: Doh, Hideo
TITLE OF INVENTION: USE OF ZRK PEPTIDE SEQUENCES IN
TITLE OF INVENTION: CONTRACEPTION
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESS: Bader & Allagretti, Ltd.
STREET: 1001 G Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20001

COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC DOS/MS-DOS
SOFTWARE: FASTSP Release #1.0 VARS. 01.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/10166
FILING DATE:

CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/289,111
FILING DATE: 11 Aug 1994

ATTORNEY/AGENT INFORMATION:
NAME: Kagan, Sarah A.
REGISTRATION NUMBER: 32,141
REFERENCE/AGENT NUMBER: 00240,46-40
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
TELEFAX: 462-508-9299
TELEX: 97440 80MB UT

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 600 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULAR TYPE: protein
HYPOHETICAL: YES
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
PCT-US95-10166-2

Query Match 5.68; Score 65; FR 5; Length 600;
Best Local Similarity 21.18; Pctid No. 2;
Matches 57; Conservative 47; Missed 47; Gaps 14;

QY 31 ISOENKALGAPPIQWVINOV-----GRRS-----HIS-----64
DB 123 VSDPEVGRHINIVAPCIKLSATFLTGKMPSSVAVMAVGLVAVVYSATK 184
QY 61 SRIEELY-----SDQELAVIGGSGVPGVAGVAGVAGVAGVAGVAGV 212
DB 183 KRVOPTKQNAVTEHDSVAVYVAKKGFVKAATFHSLEVSTLQPKATVAVHRI 179
QY 115 DWKVRLEAVVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQV 280
DB 243 IJOK-----VAGVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQV 278
QY 171 AVEAA-----N-----VAGVQVQVQVQVQVQVQVQVQVQVQVQV 278
DB 289 LPAASVKNQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQV 294

Aug 22 15:42:57 2001

us-08-659-254-18.rail

